EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	13	(proteorhodopsin or "proteo rhodopsin")	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:30
L2	1	(proteorhodopsin or "proteo rhodopsin")	EPO	OR	ON	2006/07/26 09:26
L3	0	wo-0302351-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:28
L4	0	wo-03202351-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:28
L5	0	wo-2003202351-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:28
L6	1	wo-2003002351-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:29
L7	0	wo-03002351-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:29
L8	3424	(bacteriorhodopsin or rhodopsin)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:31
L9	2	jp-60185228-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:35

EAST Search History

L10	801019	(silica or solgel or "sol gel" or gelatin or PVA or polyvinylalcohol or agarose or agar or "polyethyene glycol" or polyethyleneglycol polyvinylpyrrolidone or polyvinylacetate or (poly adj2 (vinylalcohol or vinly acetate or (vinyl adj2 (acetate or alcohol)))))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:38
L11	814255	(silica or solgel or "sol gel" or gelatin or PVA or polyvinylalcohol or agarose or agar or "polyethyene glycol" or polyethyleneglycol polyvinylpyrrolidone or polyvinylacetate or (poly adj2 (vinylalcohol or vinyl acetate or (vinyl adj2 (acetate or alcohol)))))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:38
L12	2370	l11 and l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:38
L13	97	l11 same l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:40
L14	69	l13 and @ad<"20021126"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:58
L15	639	birge	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 09:58
L16	77	birge and l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 10:01
L17	673	weetall	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 10:01
L18	18	weetall and l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 10:16

EAST Search History

L19	1	de-4224602-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 10:17
L20	2	JP-08501932-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 10:18
L21	1	1994jp-0503897.ap,prai.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/07/26 10:19

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$%^STN;HighlightOn=  ***;HighlightOff=***  ;

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 NEWS 10  JUN 02  The first reclassification of IPC codes now complete in
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FILE LAST UPDATED: 25 Jul 2006 (20060725/ED)


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=> s proteorhodopsin or proteo(2w)rhodopsin
            40 PROTEORHODOPSIN
            30 PROTEORHODOPSINS
            44 PROTEORHODOPSIN
                 (PROTEORHODOPSIN OR PROTEORHODOPSINS)
           490 PROTEO
          7470 RHODOPSIN
          5153 RHODOPSINS
          7998 RHODOPSIN
                 (RHODOPSIN OR RHODOPSINS)
             1 PROTEO(2W)RHODOPSIN
L1          45 PROTEORHODOPSIN OR PROTEO(2W)RHODOPSIN

=> d all 1-45
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L1 ANSWER 1 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2006:664836 CAPLUS <<LOGINID::20060726>>
ED Entered STN: 10 Jul 2006
TI First steps of retinal photoisomerization in ***proteorhodopsin***
AU Lenz, Martin O.; Huber, Robert; Schmidt, Bernhard; Gilch, Peter; Kalmbach, Rolf; Engelhard, Martin; Wachtveitl, Josef
CS Institut fuer Physikalische und Theoretische Chemie, Johann-Wolfgang-Goethe-Universitaet, Frankfurt, Germany
SO Biophysical Journal (2006), 91(1), 255-262
CODEN: BIOJAU; ISSN: 0006-3495
PB Biophysical Society
DT Journal
LA English
CC 6 (General Biochemistry)
AB The early steps (<1 ns) in the photocycle of the detergent solubilized proton pump ***proteorhodopsin*** are analyzed by ultrafast spectroscopic techniques. A comparison to the first primary events in reconstituted ***proteorhodopsin*** as well as to the well known archaeal proton pump bacteriorhodopsin is given. A dynamic Stokes shift obsd. in fs-time-resolved fluorescence expts. allows a direct observation of early motions on the excited state potential energy surface. The initial dynamics is dominated by sequentially emerging stretching (<150 fs) and torsional (.apprx.300 fs) modes of the retinal. The different protonation states of the primary proton acceptor Asp-97 drastically affect the reaction rate and the overall quantum efficiencies of the isomerization reactions, mainly evidenced for time scales above 1 ps. However, no major influence on the fast time scales (.apprx.150 fs) could be seen, indicating that the movement out of the Franck-Condon region is fairly robust to electrostatic changes in the retinal binding pocket. Based on fs-time-resolved absorption and fluorescence spectra, ground and exited state contributions can be disentangled and allow to construct a reaction model that consistently explains pH-dependent effects in solubilized and reconstituted ***proteorhodopsin*** .
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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AN 2006:496987 CAPLUS <<LOGINID::20060726>>
ED Entered STN: 26 May 2006
TI Strongly hydrogen-bonded water molecule is observed only in the alkaline form of ***proteorhodopsin***
AU Furutani, Yuji; Ikeda, Daisuke; Shibata, Mikihiro; Kandori, Hideki
CS Department of Materials Science and Engineering, Nagoya Institute of Technology, Showa-ku, Nagoya, 466-8555, Japan
SO Chemical Physics (2006), 324(2-3), 705-708
CODEN: CMPHC2; ISSN: 0301-0104
PB Elsevier B.V.
DT Journal
LA English
CC 6 (General Biochemistry)
AB ***Proteorhodopsin*** (PR), an archaeal-type rhodopsin found in marine bacteria, functions as a light-driven proton pump. The proton-pumping activity of PR is highly pH-dependent, its exact mechanism being still controversial. The present FTIR spectra are very similar at pH 10 and 5 in the 1800-900 cm-1 region, but significantly different in the 2700-2000 cm-1 region. This implies that the structure and structural changes are almost identical between the alk. and acid forms of PR except for water-contg. hydrogen-bonding network. In addn., different hydrogen-bonding strength of internal water mol. may be correlated with the pH-dependent proton-pumping activity of PR.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 3 OF 45 CAPLUS
AN 2006:403006 CAPLUS <<LOGINID::20060726>>
ED Entered STN: 03 May 2006
TI ***Proteorhodopsin*** -A new path for biological utilization of light energy in the sea
AU Jiao, Nianzhi; Feng, Fuying; Wei, Bo
CS State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen, 361005, Peop. Rep. China
SO Chinese Science Bulletin (2006), 51(8), 889-896
CODEN: CSBUEF; ISSN: 1001-6538
PB Science in China Press
DT Journal
LA English
CC 61 (Water)
AB The breakthrough of environmental genomics of marine microbes has revealed the existence of eubacterial rhodopsin in the sea, named ***proteorhodopsin*** (PR), which can take light to produce bio-energy for cell metab. Gene and protein sequence anal. and laser flash-induced photolysis expts. have validated the function of PR as light-driven proton-pump. During the pumping process, light energy is transformed into chem. gradient potential across plasma inner-membrane, the potential energy is then used to synthesize ATP. The finding of PR actually brings to light a novel pathway of sunlight utilization existing in heterotrophic eubacteria in contrast to the well-known chlorophyll-dependent photosynthesis in the sea. Since the group of PR-bearing bacteria is one of the numerically richest microorganisms on the Earth, accounting for 13% of the total in sea surface water, and with averaged cellular PR mols. of 2.5.times.104, PR-bearing bacteria are a key component not to be ignored in energy metab. and carbon cycling in the sea. Based on the understanding of current literature and our own investigation on PR in the China seas which indicated a ubiquitous presence and high diversity of PR in all the marine environments, we propose a conceptual model of energy flow and carbon cycling driven by both pigment-dependent and-independent biol. utilization of light in the ocean.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 4 OF 45 CAPLUS
AN 2006:140785 CAPLUS <<LOGINID::20060726>>
DN 144:386168
ED Entered STN: 15 Feb 2006
TI ***Proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea
AU Frigaard, Niels-Ulrik; Martinez, Asuncion; Mincer, Tracy J.; De Long, Edward F.
CS Department of Civil and Environmental Engineering and Division of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SO Nature (London, United Kingdom) (2006), 439(7078), 847-850
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
CC 10-4 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 3, 6, 7
AB Planktonic Bacteria, Archaea and Eukarya reside and compete in the ocean's photic zone under the pervasive influence of light. Bacteria in this environment were recently shown to contain photoproteins called ***proteorhodopsins*** , thought to contribute to cellular energy metab. by catalyzing light-driven proton translocation across the cell membrane. So far, ***proteorhodopsin*** genes have been well documented only in proteobacteria and a few other bacterial groups. Here we report the presence and distribution of ***proteorhodopsin*** genes in Archaea affiliated with the order Thermoplasmatales, in the ocean's upper water column. The genomic context and phylogenetic relationships of the archaeal and proteobacterial ***proteorhodopsins*** indicate its probable lateral transfer between planktonic Bacteria and Archaea. About 10% of the euryarchaeotes in the photic zone contained the ***proteorhodopsin*** gene adjacent to their small-subunit rRNA. The archaeal ***proteorhodopsins*** were also found in other genomic regions, in the same or in different microbial lineages. Although euryarchaeotes were distributed throughout the water column, their ***proteorhodopsins*** were found only in the photic zone. The cosmopolitan phylogenetic distribution of ***proteorhodopsins*** reflects their significant light-dependent fitness contributions, which drive the photoprotein's lateral acquisition and retention, but constrain its dispersal to the photic zone.
ST marine planktonic bacteria Archaea ***proteorhodopsin*** gene transfer phylogeny; gene pop ***proteorhodopsin*** rDNA fosmid sequence marine

bacteria
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(16 S rRNA; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S, gene; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ferredoxins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(4-iron, 4fe-4s, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ABC (ATP-binding cassette) transporters, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ABC (ATP-binding cassette) transporters, sulfate/Molybdate, Atpase component, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L13P, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L14, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L15, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L18, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L18E, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L19, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L2, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L22, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L23, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L24, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L29, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L3, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L30, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L32, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L4, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L5, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L6, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(MoeA, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Nudix domain-contg., sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(RNA helicase, ATP-dependent, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(RNA methylase-like; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S14, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S17, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(S19, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S3, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S4, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S5, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S8, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S9P, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Translation initiation factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SUI1, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Tpr repeat-like, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Trab/PrgY, -like; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(domain repeat, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Transformation, genetic
(lateral; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT RNA processing factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(mRNA, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(membrane, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Evolution
(mol.; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nrdA; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(pop; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(preprotein transporter, subunit SecY, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(proline-rich, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Protein sequences
(***proteorhodopsin*** and other encoded proteins in marine planktonic bacteria; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Genetic mapping
Marine bacteria
(***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** , sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(redox, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(secY; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(secreted, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(sulfate transporter, substrate-binding-like protein, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(threonine transporter, threonine efflux, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(transmembrane, sequence homolog; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Euryarchaeota
(uncultured marine group II or III; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT Organisms
(uncultured; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT DNA sequences
(within marine planktonic bacterial genomes; ***proteorhodopsin*** lateral gene transfer between marine planktonic Bacteria and Archaea)

IT 9029-38-3, Sulfite oxidase 9030-25-5, Orotate phosphoribosyltransferase 9032-66-0, NAD kinase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(-like; ***proteorhodopsin*** lateral gene transfer between marine

planktonic Bacteria and Archaea)
IT 81611-73-6, DNA Excinuclease
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(ATPase subunit, sequence homolog; ***proteorhodopsin*** lateral
gene transfer between marine planktonic Bacteria and Archaea)
IT 9014-24-8, RNA polymerase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(DNA-directed, sequence homolog; ***proteorhodopsin*** lateral gene
transfer between marine planktonic Bacteria and Archaea)
IT 64885-96-7, Primase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(DnaG, sequence homolog; ***proteorhodopsin*** lateral gene
transfer between marine planktonic Bacteria and Archaea)
IT 9032-84-2, Phosphoribosylformylglycinamidine synthase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(I and II, sequence homolog; ***proteorhodopsin*** lateral gene
transfer between marine planktonic Bacteria and Archaea)
IT 9033-25-4, Methyltransferase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(SAM-dependent, sequence homolog; ***proteorhodopsin*** lateral
gene transfer between marine planktonic Bacteria and Archaea)
IT 9047-64-7, Ribonucleotide reductase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(alpha subunit, sequence homolog; ***proteorhodopsin*** lateral
gene transfer between marine planktonic Bacteria and Archaea)
IT 882557-51-9 882557-52-0 882557-53-1 882557-54-2 882557-55-3
882557-56-4 882557-57-5 882557-58-6 882557-59-7 882557-60-0
882557-61-1 882557-62-2 882557-63-3 882557-64-4 882557-65-5
882557-66-6 882557-67-7 882557-68-8 882557-69-9 882557-70-2
882557-71-3 882557-72-4 882557-73-5 882557-74-6 882557-75-7
882557-76-8 882557-77-9 882557-78-0 882557-79-1 882557-80-4
882557-81-5 882557-82-6 882557-83-7 882557-84-8 882557-86-0
882557-87-1 882557-88-2 882557-89-3 882557-90-6 882557-91-7
882557-92-8 882557-93-9 882557-94-0 882557-95-1 882557-96-2
882557-97-3 882557-98-4 882557-99-5 882558-00-1 882558-01-2
882558-02-3 882558-03-4 882558-04-5 882558-05-6 882558-06-7
882558-07-8 882558-08-9 882558-09-0 882558-10-3 882558-11-4
882558-12-5 882558-13-6 882558-14-7 882558-15-8 882558-16-9
882558-17-0 882558-19-2 882558-20-5 882558-21-6 882558-22-7
882558-23-8 882558-24-9 882558-25-0 882558-26-1 882558-27-2
882558-28-3 882558-29-4 882558-30-7 882558-31-8 882558-32-9
882558-33-0 882558-34-1 882558-35-2 882558-36-3 882558-37-4
882558-38-5 882558-39-6 882558-40-9 882558-41-0 882558-42-1
882558-43-2 882558-44-3 882558-46-5 882558-47-6 882558-48-7
882558-49-8 882558-50-1 882558-51-2 882558-52-3 882558-53-4
882558-54-5 882558-55-6 882558-56-7 882558-57-8 882558-58-9
882558-59-0 882558-60-3 882558-61-4 882558-62-5 882558-63-6
882558-64-7 882558-65-8 882558-66-9 882558-67-0 882558-68-1
882558-69-2 882558-70-5 882558-71-6 882558-72-7 882558-73-8
882558-74-9 882558-75-0 882558-76-1 882558-77-2 882558-78-3
882558-79-4 882558-80-7 882558-81-8 882558-82-9 882558-83-0
882558-84-1 882558-85-2 882558-86-3 882558-87-4 882558-88-5
882558-89-6 882559-96-8 882559-98-0 882560-00-1 882560-02-3
882560-04-5 882560-06-7 882560-08-9 882560-10-3 882560-12-5
882560-14-7 882560-16-9 882560-18-1 882560-20-5 882560-22-7
882560-24-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; ***proteorhodopsin*** lateral gene transfer
between marine planktonic Bacteria and Archaea)
IT 37217-33-7, DNA polymerase III
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(exonuclease domain, sequence homolog; ***proteorhodopsin***
lateral gene transfer between marine planktonic Bacteria and Archaea)
IT 9027-41-2, Hydrolase

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(metal-dependent, sequence homolog; ***proteorhodopsin*** lateral
gene transfer between marine planktonic Bacteria and Archaea)

IT 882557-15-5 882557-16-6 882557-17-7 882557-18-8 882557-19-9
882557-20-2 882557-21-3 882557-22-4 882557-23-5 882557-24-6
882557-25-7 882557-26-8 882557-27-9 882557-28-0 882557-29-1
882557-30-4 882557-31-5 882557-32-6 882557-33-7 882557-34-8
882557-35-9 882557-36-0 882557-37-1 882557-38-2 882557-39-3
882557-40-6 882557-41-7 882557-42-8 882557-43-9 882557-44-0
882557-45-1 882557-46-2 882557-47-3 882557-48-4 882557-49-5
882557-50-8 882557-85-9 882558-18-1 882558-45-4 882558-90-9
882558-91-0 882558-92-1 882558-93-2 882558-94-3 882558-95-4
882558-96-5 882558-97-6 882558-98-7 882558-99-8 882559-00-4
882559-01-5 882559-02-6 882559-03-7 882559-04-8 882559-05-9
882559-06-0 882559-07-1 882559-08-2 882559-09-3 882559-10-6
882559-11-7 882559-12-8 882559-13-9 882559-14-0 882559-15-1
882559-16-2 882559-17-3 882559-18-4 882559-19-5 882559-20-8
882559-21-9 882559-22-0 882559-23-1 882559-24-2 882559-25-3
882559-26-4 882559-27-5 882559-28-6 882559-29-7 882559-30-0
882559-31-1 882559-32-2 882559-33-3 882559-34-4 882559-35-5
882559-36-6 882559-37-7 882559-38-8 882559-39-9 882559-40-2
882559-41-3 882559-42-4 882559-43-5 882559-44-6 882559-45-7
882559-46-8 882559-47-9 882559-48-0 882559-49-1 882559-50-4
882559-51-5 882559-52-6 882559-53-7 882559-54-8 882559-55-9
882559-56-0 882559-57-1 882559-58-2 882559-59-3 882559-60-6
882559-61-7 882559-62-8 882559-63-9 882559-64-0 882559-65-1
882559-66-2 882559-67-3 882559-68-4 882559-69-5 882559-70-8
882559-71-9 882559-72-0 882559-73-1 882559-74-2 882559-75-3
882559-76-4 882559-77-5 882559-78-6 882559-79-7 882559-80-0
882559-81-1 882559-82-2 882559-83-3 882559-84-4 882559-85-5
882559-86-6 882559-87-7 882559-88-8 882559-89-9 882559-90-2
882559-91-3 882559-92-4 882559-93-5 882559-94-6 882559-95-7
882559-97-9 882559-99-1 882560-01-2 882560-03-4 882560-05-6
882560-07-8 882560-09-0 882560-11-4 882560-13-6 882560-15-8
882560-17-0 882560-19-2 882560-21-6 882560-23-8
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence; ***proteorhodopsin*** lateral gene transfer
between marine planktonic Bacteria and Archaea)

IT 63952-00-1, .alpha.-Agarase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(precursor; ***proteorhodopsin*** lateral gene transfer between
marine planktonic Bacteria and Archaea)

IT 71427-00-4, Ribonuclease P
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(protein component 1, sequence homolog; ***proteorhodopsin***
lateral gene transfer between marine planktonic Bacteria and Archaea)

IT 37259-52-2, NAD-dependent DNA ligase 116515-35-6, Heterodisulfide
reductase 128172-71-4, Heterodisulfide reductase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(***proteorhodopsin*** lateral gene transfer between marine
planktonic Bacteria and Archaea)

IT 9001-58-5, Isocitrate dehydrogenase 9023-35-2, Pseudouridylate synthase
9024-57-1, Aspartate decarboxylase 9027-46-7, Acetyl-CoA
acetyltransferase 9030-97-1, 3-Isopropylmalate dehydrogenase
9031-26-9, Lysyl-tRNA synthetase 9031-96-3, Peptidase 9032-02-4,
Phosphoribosylglycinamide formyltransferase 9055-61-2, Dihydropteroate
synthase 37277-84-2, Cobalamin adenosyltransferase 37290-70-3, DNA
photolyase 37292-90-3, Dioxygenase 39369-30-7, RRNA methylase
58943-36-5, Thioesterase 81669-70-7, Metallopeptidase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(sequence homolog; ***proteorhodopsin*** lateral gene transfer
between marine planktonic Bacteria and Archaea)

IT 37233-48-0, Carbamoylphosphate synthase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(small and large subunits, sequence homolog; ***proteorhodopsin***

lateral gene transfer between marine planktonic Bacteria and Archaea)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 5 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2006:55279 CAPLUS <<LOGINID::20060726>>
DN 144:166099
ED Entered STN: 20 Jan 2006
TI Structure, Function, and Wavelength Selection in Blue-Absorbing ***Proteorhodopsin***

AU Hillebrecht, Jason R.; Galan, Jhenny; Rangarajan, Rekha; Ramos, Lavoisier; McCleary, Kristina; Ward, Donald E.; Stuart, Jeffrey A.; Birge, Robert R.
CS Departments of Chemistry and Molecular and Cell Biology, University of Connecticut, Storrs, CT, 06269-3060, USA

SO Biochemistry (2006), 45(6), 1579-1590
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
CC 6-3 (General Biochemistry)

AB The absorption max. of blue ***proteorhodopsin*** (BPR) is the most blue-shifted of all retinal proteins found in archaea or bacteria, with the exception of sensory rhodopsin II (SRII). The absorption spectrum also exhibits a pH dependence larger than any other retinal protein. We examine the structural origins of these two properties of BPR by using optical spectroscopy, homol. modeling, and MO theory. Bacteriorhodopsin (BR) and SRII are used as homol. parents for comparative purposes. We find that the tertiary structure of BPR based on SRII is more realistic with respect to free energy, dynamic stability, and spectroscopic properties. MO calcns. including full single- and double-CI within the chromophore .pi.-electron system provide perspectives on the wavelength regulation in this protein and indicate that Arg-95, Gln-106, Glu-143, and Asp-229 play important, and in some cases pH-dependent, roles. A possible model for the 0.22 eV red shift of BPR at low pH is examd., in which Glu-143 becomes protonated and releases Arg-95 to rotate up into the binding site, altering the electrostatic environment of the chromophore. At high pH, BPR has spectroscopic properties similar to SRII, but at low pH, BPR has spectroscopic properties more similar to BR. Nevertheless, SRII is a significantly better homol. model for BPR and opens up the question of whether this protein serves as a proton pump, as commonly believed, or is a light sensor with structure-function properties more comparable to those of SRII. The function of BPR in the native organism

is discussed with ref. to the results of the homol. model.
ST ***proteorhodopsin*** blue absorption wavelength regulation SRII homol model
IT Protonation
(Glu143; SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Chromophores
(SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Molecular orbital
(calcns.; SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Protein sequences
(homol.; SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Bacteriorhodopsins
RL: PRP (Properties)
(phoborhodopsins, SRII; SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Conformation
Tertiary structure
(protein; SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** , BPR (blue-absorbing ***proteorhodopsin***); SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(proton pump; SRII-based homol. modeling addresses wavelength regulation of BPR chromophore and suggests BPR has proton pump activity)
IT 56-84-8, L-Aspartic acid, biological studies 56-85-9, L-Glutamine, biological studies 56-86-0, L-Glutamic acid, biological studies 74-79-3, L-Arginine, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(SRII-based homol. modeling addresses roles of BPR residues Arg95, Gln106, Glu143, and Asp229 in wavelength regulation of BPR chromophore)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 6 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:1350774 CAPLUS <<LOGINID::20060726>>
DN 144:77689
ED Entered STN: 30 Dec 2005
TI Photochromic material comprising a ***proteorhodopsin*** apoprotein and retinal analog
IN Jensen, Rasmus B.; Kelemen, Bradley; Ward, Donald E., II; Asato, Alfred E.
PA Genencor International, Inc., USA; Dow Corning
SO PCT Int. Appl., 35 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM F21V009-00
CC 73-11 (Optical, Electron, and Mass Spectroscopy and Other Related Properties)
Section cross-reference(s): 6
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2005124230	A1	20051229	WO 2005-US20900	20050609

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI	US 2004-579180P	P	20040610
	US 2004-622425P	P	20041026

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2005124230	ICM	F21V009-00
	IPCI	F21V0009-00 [ICM,7]
	ECLA	A61K031/07+M; A61K031/19+M; A61K031/20+M; A61K031/215+M; A61K031/275+M; A61K038/17A2+M; C07C047/225; C07C047/24; C07C047/548; C07C175/00A4; C07C175/00A4B; G02B005/23

GI

/ Structure 1 in file .gra /

AB The present invention relates to a photochromic material comprising a ***proteorhodopsin*** apoprotein and a retinal analog. In one embodiment, the retinal analog is an azulenic retinoid compd. I [R1,R2,R3 = H, C1-4 straight or branched alkyl; n = 1 -4; X1, X2 = H, C1-4 alkyl, F, Cl or CF3; Y = direct bond, p-, m-, or o-phenyl; Z = CHO]. In another embodiment, the retinal analog is other compd. that is structurally similarly to all-trans-retinal. The ***proteorhodopsin*** apoprotein and the retinal analog form a photochromic material having different spectral properties from those of a corresponding photochromic material formed by the same ***proteorhodopsin*** apoprotein and all-trans-retinal. In one embodiment of the application, the retinal analog-contg. ***proteorhodopsin*** has an absorbance spectrum that does not overlap significantly with that of all-trans-retinal-contg. ***proteorhodopsin*** . In another embodiment of the application, the retinal analog-contg. ***proteorhodopsin*** yields a red shifted visual chromophore compared with the all-trans-retinal-contg. ***proteorhodopsin*** chromophore. The photochromic material of the present invention is useful as an optical data storage carrier, a

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     fraud-proof optical data carrier, security ink, and in other optical
     applications.
ST   photochromic material   ***proteorhodopsin***   apoprotein azulenic
     retinoid optical recording
IT   Proteins
     RL: DEV (Device component use); USES (Uses)
        (apoproteins; photochromic material comprising a
          ***proteorhodopsin***   apoprotein and retinal analog)
IT   Optical recording
     Photochromic materials
        (photochromic material comprising a   ***proteorhodopsin***
        apoprotein and retinal analog)
IT   Retinoids
     RL: DEV (Device component use); USES (Uses)
        (photochromic material comprising a   ***proteorhodopsin***
        apoprotein and retinal analog)
IT   Rhodopsins
     RL: DEV (Device component use); USES (Uses)
        (  ***proteorhodopsins***  ; photochromic material comprising a
          ***proteorhodopsin***   apoprotein and retinal analog)
IT   116-31-4, all-trans-Retinal   94756-71-5   137811-17-7   259192-39-7
     RL: DEV (Device component use); USES (Uses)
        (photochromic material comprising a   ***proteorhodopsin***
        apoprotein and retinal analog)
RE.CNT  5     THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L1   ANSWER 7 OF 45  CAPLUS  COPYRIGHT 2006 ACS on STN
AN   2005:1350735  CAPLUS &lt;&lt;LOGINID::20060726&gt;&gt;
DN   144:97744
ED   Entered STN:  30 Dec 2005
TI   Compositions comprising various   ***proteorhodopsins***   and/or
     bacteriorhodopsins and use thereof for photochromic information carrier
IN   Bott, Richard R.; Jensen, Rasmus B.; Kelemen, Bradley; Ward, Donald E.,
     II; Whited, Gregory M.
PA   Genencor International, Inc., USA; Dow Corning
SO   PCT Int. Appl., 36 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
IC   ICM  A61K038-17
     ICS  C07K014-705
CC   74-9 (Radiation Chemistry, Photochemistry, and Photographic and Other
     Reprographic Processes)
     Section cross-reference(s): 11
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     PATENT NO.          KIND   DATE       APPLICATION NO.        DATE
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PI   WO 2005123110        A2    20051229   WO 2005-US20899        20050609
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             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ,
             LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA,
             NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK,
             SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU,
             ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM,
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             EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT,
             RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML,
             MR, NE, SN, TD, TG
PRAI US 2004-579181P      P      20040610
     US 2004-622424P      P      20041026
CLASS
 PATENT NO.       CLASS  PATENT FAMILY CLASSIFICATION CODES
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 WO 2005123110    ICM    A61K038-17
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ICS C07K014-705
IPCI A61K0038-17 [ICM,7]; C07K0014-705 [ICS,7]; C07K0014-435 [ICS,7,C*]
ECLA C07K014/215

AB The present invention provides a solid material comprising an immobilized mixt. of two or more ***proteorhodopsins*** , two or more bacteriorhodopsins, or one or more bacteriorhodopsin and one or more ***proteorhodopsins*** . The ***proteorhodopsins*** are selected from the group consisting of all-trans-retinal-contg. ***proteorhodopsins*** and retinal analog-contg. ***proteorhodopsins*** ; all of which have absorption spectra that do not overlap. The bacteriorhodopsins are selected from the group consisting of all-trans-retinal- contg. bacteriorhodopsins and retinal analog-contg. bacteriorhodopsins; all of which have absorption spectra that do not overlap. The present invention also provides an optical information carrier, such as an optical data storage material and a fraud-proof optical data carrier, comprising the above-described solid material and a substrate selected from the group consisting of glass, paper, metal, fabric material, and plastic material, wherein said solid material is deposited on said substrate. The present invention further provides security ink comprising one or more hydrophilic polymers and a mixt. of various photochromic materials.

ST optical recording material ***proteorhodopsin*** bacteriorhodopsin compn security ink photochromic

IT Optical recording materials
Photochromic materials
(compns. comprising various ***proteorhodopsins*** and/or bacteriorhodopsins and use thereof for optical information carrier)

IT Bacteriorhodopsins
RL: TEM (Technical or engineered material use); USES (Uses)
(compns. comprising various ***proteorhodopsins*** and/or bacteriorhodopsins and use thereof for optical information carrier)

IT Rhodopsins
RL: TEM (Technical or engineered material use); USES (Uses)
(***proteorhodopsins*** ; compns. comprising various ***proteorhodopsins*** and/or bacteriorhodopsins and use thereof for optical information carrier)

IT Information systems
(security documents; compns. comprising various ***proteorhodopsins*** and/or bacteriorhodopsins and use thereof for optical information carrier)

L1 ANSWER 8 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:1338047 CAPLUS <<LOGINID::20060726>>
DN 144:32716
ED Entered STN: 25 Dec 2005
TI The genome of Salinibacter ruber: Convergence and gene exchange among hyperhalophilic bacteria and archaea
AU Mongodin, E. F.; Nelson, K. E.; Daugherty, S.; DeBoy, R. T.; Wister, J.; Khouri, H.; Weidman, J.; Walsh, D. A.; Papke, R. T.; Perez, G. Sanchez; Sharma, A. K.; Nesbo, C. L.; MacLeod, D.; Bapteste, E.; Doolittle, W. F.; Charlebois, R. L.; Legault, B.; Rodriguez-Valera, F.
CS The Institute for Genomic Research, Rockville, MD, 20850, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2005), 102(50), 18147-18152
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 10

AB Satd. thalassic brines are among the most phys. demanding habitats on Earth: few microbes survive in them. Salinibacter ruber is among these organisms and has been found repeatedly in significant nos. in climax saltern crystallizer communities. The phenotype of this bacterium is remarkably similar to that of the hyperhalophilic Archaea (Haloarchaea). The genome sequence suggests that this resemblance has arisen through convergence at the physiol. level (different genes producing similar overall phenotype) and the mol. level (independent mutations yielding similar sequences or structures). Several genes and gene clusters also derive by lateral transfer from (or may have been laterally transferred to) haloarchaea. S. ruber encodes four rhodopsins. One resembles

bacterial ***proteorhodopsins*** and three are of the haloarchaeal type, previously uncharacterized in a bacterial genome. The impact of these modular adaptive elements on the cell biol. and ecol. of S. ruber is substantial, affecting salt adaptation, bioenergetics, and photobiol. The complete genome sequence of S. ruber strain M31T DSM13855 is deposited in GenBank/EMBL/DDBJ under accession nos. CP000159 (chromosome) and CP000160 (plasmid pSR35).

ST Salinibacter ruber genome proteome sequence; gene sequence Salinibacter ruber genome; protein sequence Salinibacter ruber genome; adaptation salinity Salinibacter genome sequence

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(SR-I (sensory rhodopsin I); complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Adaptation, microbial
Archaea
DNA sequences
Genome
Protein sequences
Salinibacter ruber
Salinity
(complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Gene, microbial
Proteins
Proteome
Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(halorhodopsins; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Eubacteria
(hyperhalophilic; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Evolution
(mol.; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(phoborhodopsins; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT 870956-89-1 870956-90-4 870956-91-5 870956-92-6 870956-93-7
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT 116-31-4, Retinal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

IT 870930-81-7 870958-83-1, DNA (plasmid pSR35)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; complete genome sequence of Salinibacter ruber demonstrates convergence and gene exchange among hyperhalophilic bacteria and archaea)

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AN 2005:1170820 CAPLUS <<LOGINID::20060726>>
DN 144:66604
ED Entered STN: 03 Nov 2005
TI ***Proteorhodopsin*** in the ubiquitous marine bacterium SAR11
AU Giovannoni, Stephen J.; Bibbs, Lisa; Cho, Jang-Cheon; Stapels, Martha D.; Desiderio, Russell; Vergin, Kevin L.; Rappe, Michael S.; Laney, Samuel; Wilhelm, Lawrence J.; Tripp, H. James; Mathur, Eric J.; Barofsky, Douglas F.
CS Department of Microbiology, Oregon State University, Corvallis, OR, 97331, USA
SO Nature (London, United Kingdom) (2005), 438(7064), 82-85
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
CC 10-4 (Microbial, Algal, and Fungal Biochemistry)
AB ***Proteorhodopsins*** are light-dependent proton pumps that are predicted to have an important role in the ecol. of the oceans by supplying energy for microbial metab. ***Proteorhodopsin*** genes were first discovered through the cloning and sequencing of large genomic

DNA fragments from seawater. They were later shown to be widely distributed, phylogenetically diverse, and active in the oceans. ***Proteorhodopsin*** genes have not been found in cultured bacteria, and on the basis of environmental sequence data, it has not yet been possible to reconstruct the genomes of uncultured bacterial strains that have ***proteorhodopsin*** genes. Although the metabolic effect of ***proteorhodopsins*** is uncertain, they are thought to function in cells for which the primary mode of metab. is the heterotrophic assimilation of dissolved org. carbon. Here we report that SAR11 strain HTCC 1062 ('Pelagibacter ubique'), the first cultivated member of the extraordinarily abundant SAR11 clade, expresses a ***proteorhodopsin*** gene when cultured in autoclaved seawater and in its natural environment, the ocean. The Pelagibacter ***proteorhodopsin*** functions as a light-dependent proton pump. The gene is expressed by cells grown in either diurnal light or in darkness, and there is no difference between the growth rates or cell yields of cultures grown in light or darkness.

ST Pelagibacter ***proteorhodopsin***

IT Evolution
(mol., phylogeny; ***proteorhodopsin*** in ubiquitous marine bacterium SAR11)

IT Pelagibacter ubique
(***proteorhodopsin*** in ubiquitous marine bacterium SAR11)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsin*** in ubiquitous marine bacterium SAR11)

IT Rhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsins*** ; ***proteorhodopsin*** in ubiquitous marine bacterium SAR11)

IT Transport proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proton pump, light-dependent; ***proteorhodopsin*** in ubiquitous marine bacterium SAR11)

IT Mutation
(substitution; ***proteorhodopsin*** in ubiquitous marine bacterium SAR11)

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L1 ANSWER 10 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2005:843189 CAPLUS <<LOGINID::20060726>>

DN 143:435594

ED Entered STN: 22 Aug 2005

TI New insights into metabolic properties of marine bacteria encoding ***proteorhodopsins***

AU Sabehi, Gazalah; Loy, Alexander; Jung, Kwang-Hwan; Partha, Ranga; Spudich, John L.; Isaacson, Tal; Hirschberg, Joseph; Wagner, Michael; Beja, Oded

CS Department of Biology, Technion-Israel Institute of Technology, Haifa, Israel

SO PLoS Biology (2005), 3(8), 1409-1417
CODEN: PBLIBG; ISSN: 1545-7885

URL: http://biology.plosjournals.org/archive/1545-7885/3/8/pdf/10.1371_1545-7885_3_8_complete.pdf
PB Public Library of Science
DT Journal; (online computer file)
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)

AB ***Proteorhodopsin*** phototrophy was recently discovered in oceanic surface waters. In an effort to characterize uncultured ***proteorhodopsin*** -exploiting bacteria, large-insert bacterial artificial chromosome (BAC) libraries from the Mediterranean Sea and Red Sea were analyzed. Fifty-five BACs carried diverse ***proteorhodopsin*** genes, and we confirmed the function of 5. We calc. that ***proteorhodopsin*** -exploiting bacteria account for 13% of microorganisms in the photic zone. We further show that some ***proteorhodopsin*** -contg. bacteria possess a retinal biosynthetic pathway and a reverse sulfite reductase operon, employed by prokaryotes oxidizing sulfur compds. Thus, these novel phototrophs are an unexpectedly large and metabolically diverse component of the marine microbial surface water.

ST metab marine bacteria ***proteorhodopsin***

IT Marine bacteria
Metabolism, microbial
(metabolic properties of marine bacteria encoding ***proteorhodopsins***)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(metabolic properties of marine bacteria encoding ***proteorhodopsins***)

IT Rhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsins*** ; metabolic properties of marine bacteria encoding ***proteorhodopsins***)

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L1 ANSWER 11 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:638670 CAPLUS <<LOGINID::20060726>>
DN 143:149405
ED Entered STN: 22 Jul 2005
TI Membranes incorporating recognition moieties and thiosulfonate-activated ionophores
IN Sala, Rafael Fernando
PA Genencor International, Inc., USA
SO PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N
CC 9-1 (Biochemical Methods)
Section cross-reference(s): 2, 15
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2005065405	A1	20050721	WO 2004-US44039	20041229

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	US 2005250128	A1	20051110	US 2004-24571	20041228
PRAI	US 2003-533672P	P	20031231		
	US 2004-24571	A	20041228		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2005065405	ICM	G01N
	IPCI	G01N [ICM,7]
	IPCR	A61K0031-185 [I,A]; A61K0031-185 [I,C*]; C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-705 [I,A]; C12N0015-09 [I,A]; C12N0015-09 [I,C*]; C12P0021-06 [I,A]; C12P0021-06 [I,C*]; C12Q0001-68 [I,A]; C12Q0001-68 [I,C*]
US 2005250128	IPCI	C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12P0021-06 [ICS,7]; C12N0015-09 [ICS,7]; C07K0014-705 [ICS,7]; C07K0014-435 [ICS,7,C*]; A61K0031-185 [ICS,7]
	IPCR	A61K0031-185 [I,A]; A61K0031-185 [I,C*]; C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-705 [I,A]; C12N0015-09 [I,A]; C12N0015-09 [I,C*]; C12P0021-06 [I,A]; C12P0021-06 [I,C*]; C12Q0001-68 [I,A]; C12Q0001-68 [I,C*]
	NCL	435/006.000

AB The present invention provides a thiosulfonate-activated ionophore comprising an ionophore, a spacer group, and an alkylthiosulfonate moiety. A preferred ionophore is gramicidin A. A preferred alkylthiosulfonate is methanethiosulfonate. The present invention also provides a conjugate comprising an ionophore, a spacer group, and a recognition mol. Further the invention related to membranes incorporating the conjugates and biosensors comprising said membranes. A gramicidin-Fab antibody conjugate targeting human chorionic gonadotropin was prepd. and incorporated into a membrane on an electrode. The sensor was used to detect human chorionic gonadotropin.
ST membrane thiosulfonate activated ionophore recognition mol; biosensor membrane thiosulfonate activated ionophore reagent; gramicidin antibody conjugate membrane biosensor chorionic gonadotropin
IT Functional groups

(alkoxycarbonyl groups, as spacer; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Functional groups
(alkylidene glycol oligomers, as spacer; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Amphoteric materials
(amphiphilic, membrane comprising; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Samples
(anal. of; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Alkyl groups
Amide group
(as spacer; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Oligopeptides
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(as spacer; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Transport proteins
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(band 3, thiosulfonate-activated; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Analytical apparatus
(biochem., biosensors array in; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Biosensors
Electric conductors
Electrodes
Human
Membranes, nonbiological
(biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Functional groups
(carbamates, as spacer; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Aptamers
Chelating agents
Dyes
(conjugates with ionophore; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Agglutinins and Lectins
Antibodies and Immunoglobulins
Antigens
Enzymes, biological studies
Haptens
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DEV (Device component use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(conjugates, with ionophore; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Electric impedance
(detn. of change in; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Ions
(flow across membrane, analyte causing change in; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DEV (Device component use); SPN (Synthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(fragments, conjugates with ionophore; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT Biosensors

(immunosensors; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Disulfide group
(linking ionophore and recognition mol.; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Phospholipids, uses
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(membrane comprising; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Flow
(of ions across membrane, analyte causing change in; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Self-assembled monolayers
(of lipids contg. ionophore on gold-covered slide; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Rhodopsins
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(***proteorhodopsins*** , thiosulfonate-activated; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Ionophores
(thiosulfonate-activated; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT Bacteriorhodopsins
Porins
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(thiosulfonate-activated; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT 859230-14-1DP, reaction with gramicidins 859230-15-2DP, reaction with gramicidins
RL: ARG (Analytical reagent use); DEV (Device component use); RCT (Reactant); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(as activated ionophore; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT 107-21-1D, Ethylene glycol, oligomers with amides, esters or carbamates
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(as spacer; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT 9002-61-3, Chorionic gonadotropin
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT 1393-88-0D, Gramicidin D, thiosulfonate-activated 1404-88-2D, Tyrothricin, thiosulfonate-activated 1405-97-6D, Gramicidin, thiosulfonate-activated 2001-95-8D, Valinomycin, thiosulfonate-activated 8011-61-8D, Tyrocidine, thiosulfonate-activated 9062-60-6D, Gramicidin B, thiosulfonate-activated 9062-61-7D, Gramicidin C, thiosulfonate-activated 9066-06-2D, Gramicidin A', thiosulfonate-activated 27061-78-5D, Alamethicin, thiosulfonate-activated, analogs 37231-28-0D, Melittin, thiosulfonate-activated 859504-00-0D, Gramicidin GT, thiosulfonate-activated 859504-01-1D, Gramicidin GM, thiosulfonate-activated 859504-05-5D, Gramicidin GM-, thiosulfonate-activated 859504-07-7D, Gramicidin GN-, thiosulfonate-activated
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)

IT 11029-61-1DP, Gramicidin A, thiosulfonate-activated, conjugates with Fab' antibody
RL: ARG (Analytical reagent use); DEV (Device component use); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)

(biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT 108-30-5, Succinic anhydride, reactions 1393-88-0, Gramicidin D 1950-85-2, Sodium Methanethiosulfonate 4224-70-8, 6-Bromohexanoic acid 4246-51-9, 4,7,10-Trioxa-1,13-tridecanediamine 6066-82-6 7693-46-1, p-Nitrophenyl chloroformate 14254-46-7D, reaction with gramicidins 61792-23-2, Bromobutyric acid 194920-62-2 756525-91-4 859230-16-3D, reaction product with gramicidins
RL: RCT (Reactant); RACT (Reactant or reagent)
(biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT 14254-46-7DP, reaction product with gramicidins 42014-54-0P 76078-72-3P 76078-81-4P 690632-55-4P 859230-17-4DP, reaction product with gramicidins 859230-18-5P 859230-19-6P 859230-20-9P 859230-21-0P 859230-22-1P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT 99341-19-2, 1,2-Di-O-phytanyl-sn-glycerol 207131-40-6
RL: DEV (Device component use); USES (Uses)
(in second layer lipids in membrane on electrode; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT 44059-82-7, Methanesulfonothioic acid
RL: ARG (Analytical reagent use); DEV (Device component use); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(ionophore activated with; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT 13686-28-7, Thiosulfuric acid ($H_2S_2O_3$) 13686-28-7D, Thiosulfuric acid ($H_2S_2O_3$), compds.
RL: RCT (Reactant); RACT (Reactant or reagent)
(ionophore activated with; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
IT 7440-57-5, Gold, uses
RL: DEV (Device component use); USES (Uses)
(slide covered with; biosensors and membranes incorporating recognition moieties and thiosulfonate-activated ionophores)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Cornell; US 5874316 A 1999 CAPLUS

L1 ANSWER 12 OF 45 CAPLUS
AN 2005:629397 CAPLUS <<LOGINID::20060726>>
DN 143:168224
ED Entered STN: 20 Jul 2005
TI Role of conserved arginine in solar energy conversion: Infrared spectroscopy of bacteriorhodopsin, ***proteorhodopsin*** , and model compounds
AU Xiao, Yaowu
CS Syracuse Univ., Syracuse, NY, USA
SO (2004) 137 pp. Avail.: UMI, Order No. DA3138876
From: Diss. Abstr. Int., B 2005, 65(7), 3454
DT Dissertation; General Review
LA English
CC 6-0 (General Biochemistry)
AB Unavailable
ST review solar energy conversion IR spectroscopy arginine ***proteorhodopsin*** bacteriorhodopsin
IT Solar energy
(conversion; role of conserved arginine in solar energy conversion: IR spectroscopy of bacteriorhodopsin, ***proteorhodopsin*** , and model compds.)
IT Rhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsins*** ; role of conserved arginine in solar energy conversion: IR spectroscopy of bacteriorhodopsin, ***proteorhodopsin*** , and model compds.)
IT IR spectroscopy
(role of conserved arginine in solar energy conversion: IR spectroscopy of bacteriorhodopsin, ***proteorhodopsin*** , and model compds.)

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(role of conserved arginine in solar energy conversion: IR spectroscopy of bacteriorhodopsin, ***proteorhodopsin*** , and model compds.)
IT 74-79-3, Arginine, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(role of conserved arginine in solar energy conversion: IR spectroscopy of bacteriorhodopsin, ***proteorhodopsin*** , and model compds.)

L1 ANSWER 13 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:621829 CAPLUS <<LOGINID::20060726>>
DN 143:243696
ED Entered STN: 19 Jul 2005
TI Formation of a Long-Lived Photoproduct with a Deprotonated Schiff Base in ***Proteorhodopsin*** , and Its Enhancement by Mutation of Asp227
AU Imasheva, Eleonora S.; Shimono, Kazumi; Balashov, Sergei P.; Wang, Jennifer M.; Zadok, Uri; Sheves, Mordechai; Kamo, Naoki; Lanyi, Janos K.
CS Department of Physiology and Biophysics, University of California, Irvine, CA, 92697, USA
SO Biochemistry (2005), 44(32), 10828-10838
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
CC 6-3 (General Biochemistry)
Section cross-reference(s): 74
AB ***Proteorhodopsin*** , a retinal protein of marine proteobacteria similar to bacteriorhodopsin of the archaea, is a light-driven proton pump. Absorption of a light quantum initiates a reaction cycle (turnover time of .apprx.50 ms), which includes photoisomerization of the retinal from the all-trans to the 13-cis form and transient deprotonation of the retinal Schiff base, followed by recovery of the initial state. We report here that in addn. to this fast cyclic conversion, illumination at high pH results in accumulation of a long-lived photoproduct absorbing at 362 nm. This photoconversion is much more efficient in the D227N mutant in which the anionic Asp227, which together with Asp97 constitutes the Schiff base counterion, is replaced with a neutral residue. Upon illumination at pH 8.5, most of the D227N pigment is converted to the 362 nm species, with a quantum efficiency of .apprx.0.2. The pKa for this transition in the wild type is 9.6, but decreased to 7.5 after mutation of Asp227. The short wavelength of the absorption max. of the photoproduct indicates that it has a deprotonated Schiff base. In the dark, this photoproduct is converted back to the initial pigment with a time const. of 30 min (in D227N, at pH 8.5), but it can be reconverted more rapidly by illumination with near-UV light. Expts. with "locked" retinal analogs which selectively exclude rotation around either the C9:C10, C11:C12, or C13:C14 bond show that formation of the 362 nm species involves isomerization around the C13:C14 bond. In agreement with this, retinal extn. indicates that the 362 nm photoproduct is 13-cis whereas the initial state is predominantly all-trans. A rapid shift of the pH from 8.5 to 4 greatly accelerates thermal reconversion of the 362 nm species to the initial pigment, suggesting that its recovery involving the thermal isomerization of the chromophore is controlled by ionizable residues, primarily the Schiff base and Asp97. The transformation to the long-lived 362 nm photoproduct is apparently a side reaction of the photocycle, a response to high pH, caused by alteration of the normal reprotonation and reisomerization pathway of the Schiff base.
ST ***proteorhodopsin*** rhodopsin photoisomerization Schiff base
IT Schiff bases
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); BIOL (Biological study); PROC (Process)
(formation of long-lived photoproduct with deprotonated Schiff base in ***proteorhodopsin*** , and its enhancement by mutation of Asp227)
IT Isomerization
(photoisomerization; formation of long-lived photoproduct with deprotonated Schiff base in ***proteorhodopsin*** , and its enhancement by mutation of Asp227)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); BIOL (Biological study); PROC (Process)

(***proteorhodopsins*** ; formation of long-lived photoproduct with deprotonated Schiff base in ***proteorhodopsin*** , and its enhancement by mutation of Asp227)

IT 34372-62-8 863394-09-6 863394-10-9 863394-11-0
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); BIOL (Biological study); PROC (Process)
(photoreaction of; formation of long-lived photoproduct with deprotonated Schiff base in ***proteorhodopsin*** , and its enhancement by mutation of Asp227)

RE.CNT 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 14 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:620517 CAPLUS <<LOGINID::20060726>>
DN 143:207915
ED Entered STN: 18 Jul 2005
TI Biochemical characterization of ***proteorhodopsin***
AU Parthasarathy, Rangadorai D.
CS Syracuse Univ., Syracuse, NY, USA
SO (2004) 112 pp. Avail.: UMI, Order No. DA3135882
From: Diss. Abstr. Int., B 2004, 65(6), 2925
DT Dissertation
LA English
CC 6-3 (General Biochemistry)
AB Unavailable
ST ***proteorhodopsin*** conformation
IT Conformation
(protein; biochem. characterization of ***proteorhodopsin***)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; biochem. characterization of ***proteorhodopsin***)

L1 ANSWER 15 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:588425 CAPLUS <<LOGINID::20060726>>
DN 143:74518
ED Entered STN: 08 Jul 2005
TI Rapid and inexpensive method for the purification of ***proteorhodopsin***
IN Braiman, Mark S.; Partha, Ranga
PA USA
SO U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DT Patent
LA English
IC ICM C07K014-705
INCL 530350000; 530412000
CC 9-16 (Biochemical Methods)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2005148762	A1	20050707	US 2004-886782	20040707
PRAI	US 2003-485272P	P	20030707		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 2005148762	ICM	C07K014-705
	INCL	530350000; 530412000
	IPCI	C07K0014-705 [ICM,7]; C07K0014-435 [ICM,7,C*]
	IPCR	C07K0014-195 [I,A]; C07K0014-195 [I,C*]; C07K0014-435 [I,C*]; C07K0014-705 [I,A]
	NCL	530/350.000
	ECLA	C07K014/195; C07K014/705

AB A method for purifying a membrane protein is disclosed which includes providing a test sample potentially including a target membrane protein; adding incremental amts. of a pptg. agent to the test sample to form one or more mixts.; and treating the one or more mixts. under conditions effective to obtain pptd., purified target membrane protein if present in the test sample.
ST inexpensive purifn ***proteorhodopsin***
IT Proteins
RL: PUR (Purification or recovery); PREP (Preparation)
(membrane; method for purifn. of ***proteorhodopsin***)
IT G protein-coupled receptors
RL: PUR (Purification or recovery); PREP (Preparation)
(method for purifn. of ***proteorhodopsin***)
IT Rhodopsins
RL: PUR (Purification or recovery); PREP (Preparation)

(***proteorhodopsins*** ; method for purifn. of
proteorhodopsin)
IT 77-92-9, Citric acid, biological studies 9002-93-1, Triton-X100
29836-26-8
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(method for purifn. of ***proteorhodopsin***)

L1 ANSWER 16 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:510774 CAPLUS <<LOGINID::20060726>>
DN 143:188572
ED Entered STN: 15 Jun 2005
TI Weakened coupling of conserved arginine to the ***proteorhodopsin***
chromophore and its counterion implies structural differences from
bacteriorhodopsin
AU Partha, Ranga; Krebs, Richard; Caterino, Tamara L.; Braiman, Mark S.
CS Syracuse University Chemistry Department, Syracuse, NY, 13244-4100, USA
SO Biochimica et Biophysica Acta, Bioenergetics (2005), 1708(1), 6-12
CODEN: BBBEB4; ISSN: 0005-2728
PB Elsevier B.V.
DT Journal
LA English
CC 6-3 (General Biochemistry)
AB In wild-type ***proteorhodopsin*** (pR), titrn. of the chromophore's
counterion Asp97 occurs with a pK a of 8.2. R94C mutation reduces this
slightly to 7.0, irresp. of treatment with ethylguanidinium. This
contrasts with the homologous archaeal protein bacteriorhodopsin (bR),
where R82C mutation was previously shown to elevate the pKa of Asp85 by
.apprx.5 units, while reconstitution with ethylguanidinium restores it
nearly to the wild-type value of 2.5. The authors conclude there is much
weaker electrostatic coupling between Arg94 and Asp97 in the unphotolyzed
state of pR, in comparison to Arg82 and Asp85 in bR. Therefore, while
fast light-driven H+ release may depend on these two residues in pR as in
bR, no tightly conserved pre-photolysis configuration of them is required.
ST ***proteorhodopsin*** chromophore conserved arginine electrostatic
coupling counterion bacteriorhodopsin
IT Rhodopsins
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or
chemical process); PRP (Properties); PYP (Physical process); BIOL
(Biological study); PROC (Process)
(***proteorhodopsins*** ; weakened coupling of conserved arginine to
proteorhodopsin chromophore and its counterion implies
structural differences from bacteriorhodopsin)
IT Deprotonation
Electrostatic force
Photolysis
(weakened coupling of conserved arginine to ***proteorhodopsin***
chromophore and its counterion implies structural differences from
bacteriorhodopsin)
IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(weakened coupling of conserved arginine to ***proteorhodopsin***
chromophore and its counterion implies structural differences from
bacteriorhodopsin)
IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(weakened coupling of conserved arginine to ***proteorhodopsin***
chromophore and its counterion implies structural differences from
bacteriorhodopsin)
IT 56-84-8, L-Aspartic acid, biological studies 74-79-3, L-Arginine,
biological studies
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or
chemical process); PRP (Properties); PYP (Physical process); BIOL
(Biological study); PROC (Process)
(weakened coupling of conserved arginine to ***proteorhodopsin***
chromophore and its counterion implies structural differences from
bacteriorhodopsin)
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 17 OF 45 CAPLUS
AN 2005:386843 CAPLUS <<LOGINID::20060726>>
DN 144:18203
ED Entered STN: 05 May 2005
TI Kinetic isotope effects in the photochemical reaction cycle of ion transporting retinal proteins
AU Szakacs, Julianna; Lakatos, Melinda; Ganea, Constanta; Varo, Gyoergy
CS Department of Biophysics, University of Medicine and Pharmacy, Tg. Mures, Rom.
SO Journal of Photochemistry and Photobiology, B: Biology (2005), 79(2), 145-150
CODEN: JPPBEG; ISSN: 1011-1344
PB Elsevier B.V.
DT Journal
LA English
CC 6-1 (General Biochemistry)
AB The kinetics of the photochem. reaction cycle of the bacteriorhodopsin, pharaonis halorhodopsin and ***proteorhodopsin*** were detd. in H2O and D2O at low and high pH, to get insight in the proton dependent steps of the transport process. While all the steps of the bacteriorhodopsin photocycle at normal pH exhibited a strong isotope effect, the proton uptake step of the photocycle, measured at high pH, became independent of deuterium exchange, making plausible that this step, at low proton concn., becomes concn. dependent, not mobility dependent. The proton transporting photocycle of the ***proteorhodopsin*** at its normal pH (9.5) shows a marked deuterium effect, while at high pH (12.2) this effect almost totally disappears. It was shown earlier that the proton uptake step of the ***proteorhodopsin*** is at the rise of the N form. As the proton concn. decreases with rising pH this step becomes the rate limiting,

proton concn. dependent step, hiding all the other isotope dependent components. In the case of halorhodopsin in all the chloride, nitrate and proton transporting conditions the photocycle was not strongly affected by the deuterium exchange. While in the cases of the first two ions this seems normal, the absence of the deuterium effect in the case of the proton transporting photocycle was a puzzle. The only plausible explanation is that in the presence of azide the halorhodopsin transports not the proton, but a neg. charged ion the OH-, the mass and mobility of which is only slightly influenced by the deuterium exchange.

ST kinetic isotope photochem reaction ion transporting retinal protein

IT Biological transport
(chloride; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT Isotope effect
(deuterium; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(halorhodopsins; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT Biological transport
(hydrogen ion, bsu; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(retinal; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(transport, bsu; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

IT 14797-55-8, Nitrate, biological studies 16887-00-6, Chloride, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(transport; kinetic isotope effects in photochem. reaction cycle of ion transporting retinal proteins at low and high pH)

RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 18 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:36683 CAPLUS <<LOGINID::20060726>>
DN 142:256429
ED Entered STN: 16 Jan 2005
TI pH-Dependent Photoisomerization of Retinal in ***Proteorhodopsin***
AU Huber, Robert; Koehler, Thomas; Lenz, Martin O.; Bamberg, Ernst; Kalmbach, Rolf; Engelhard, Martin; Wachtveitl, Josef
CS Institut fuer Physikalische und Theoretische Chemie, Johann Wolfgang Goethe-Universitaet Frankfurt, Frankfurt am Main, 60439, Germany
SO Biochemistry (2005), 44(6), 1800-1806
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
CC 6-3 (General Biochemistry)
AB The early steps in the photocycle of the bacterial proton pump ***proteorhodopsin*** (PR) were analyzed by ultrafast pump/probe spectroscopy to compare the rate of retinal isomerization at alk. and acidic pH values. At pH 9, the functionally important primary proton acceptor (Asp97, pKa = 7.7) is neg. charged; consequently, a reaction cycle analogous to the archaeal bacteriorhodopsin (BR) is obsd. The excited electronic state of PR displays a pronounced biphasic decay with time consts. of 400 fs and 8 ps. At pH 6 where Asp97 is protonated a similar biphasic decay is obsd., although it is significantly slower (700 fs and 15 ps). The results indicate, in agreement to similar findings in other retinal proteins, that also in PR the charge distribution within the chromophore binding pocket is a major determinant for the rate and the efficiency of the primary reaction.
ST photoisomerization retina retinal ***proteorhodopsin***
IT Excited electronic state
(pH-dependent photoisomerization of retinal in ***proteorhodopsin***)
IT Isomerization
(photoisomerization; pH-dependent photoisomerization of retinal in ***proteorhodopsin***)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; pH-dependent photoisomerization of retinal in ***proteorhodopsin***)
IT Eye
(retina; role of Asp97 residue of retina ***proteorhodopsin*** in photoisomerization)
IT Proton transfer
(role of Asp97 residue of retina ***proteorhodopsin*** in photoisomerization)
IT 116-31-4, all-trans-Retinal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(pH-dependent photoisomerization of retinal in ***proteorhodopsin***)
IT 56-84-8, L-Aspartic acid, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(role of Asp97 residue of retina ***proteorhodopsin*** in photoisomerization)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN 2004:1048392 CAPLUS <<LOGINID::20060726>>
DN 142:129346
ED Entered STN: 08 Dec 2004
TI Time-Resolved FTIR Spectroscopy of the Photointermediates Involved in Fast Transient H+ Release by ***Proteorhodopsin***
AU Xiao, Yaowu; Partha, Ranga; Krebs, Richard; Braiman, Mark
CS Department of Chemistry, Syracuse University, Syracuse, NY, 13244-4100, USA
SO Journal of Physical Chemistry B (2005), 109(1), 634-641
CODEN: JPCBFK; ISSN: 1520-6106
PB American Chemical Society
DT Journal
LA English
CC 6-3 (General Biochemistry)
AB ***Proteorhodopsin*** (pR) is a homolog of bacteriorhodopsin (bR) that has been recently discovered in oceanic bacterioplankton. Like bR, pR functions as a light-driven proton pump. As previously characterized by laser flash induced absorption spectroscopy (Krebs, R. A.; Alexiev, U.; Partha, R.; DeVita, A. M.; Braiman, M. S. BMC Physiol. 2002, 2, 5), the pR photocycle shows evidence of light-induced H+ release on the 10-50 .mu.s time scale, and of substantial accumulation of the M intermediate, only at pH values above 9 and after reconstitution into phospholipid followed by extensive washing to remove detergent. We have therefore measured the time-resolved FTIR difference spectra of pR intermediates reconstituted into DMPC vesicles at pH 9.5. A mixt. of K- and L-like intermediates, characterized by a 1516 cm-1 pos. band and a 1742 cm-1 neg. band resp., appears within 20 .mu.s after photolysis. This mixt. decays to an M-like state, with a clear band at 1756 cm-1 due to protonation of Asp-97. The 50-70 .mu.s rise of M at pH 9.5 is similar to (but a little slower than)

the rise times for M formation and H+ release that were reported earlier based on flash photolysis measurements of pR reconstituted into phospholipids with shorter acyl chains. We conclude that, at pH 9.5, H+ release occurs while Asp-97 is still protonated; i.e., this aspartic acid cannot be the H+ release group obsd. by flash photolysis under similar conditions.

ST ***proteorhodopsin*** proton transfer

IT Protonation
(Asp97 residue of ***proteorhodopsin*** is not involved in proton transfer)

IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; time-resolved FTIR spectroscopy of photointermediates involved in fast transient proton release by ***proteorhodopsin***)

IT Proton transfer
(time-resolved FTIR spectroscopy of photointermediates involved in fast transient proton release by ***proteorhodopsin***)

IT 56-84-8, L-Aspartic acid, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Asp97 residue of ***proteorhodopsin*** is not involved in proton transfer)

RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 20 OF 45 CAPLUS
AN 2004:888098 CAPLUS <<LOGINID::20060726>>
DN 142:33632
ED Entered STN: 26 Oct 2004
TI Darwinian adaptation of ***proteorhodopsin*** to different light intensities in the marine environment

AU Bielawski, Joseph P.; Dunn, Katherine A.; Sabehi, Gazalah; Beja, Oded
CS Department of Biology and Department of Mathematics and Statistics, Dalhousie University, Halifax, NS, B3H 4J1, Can.
SO Proceedings of the National Academy of Sciences of the United States of America (2004), 101(41), 14824-14829
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
CC 3-6 (Biochemical Genetics)
Section cross-reference(s): 10, 20
AB ***Proteorhodopsin*** , a retinal-binding protein, represents a potentially significant source of light-driven energy prodn. in the world's oceans. The distribution of photochem. divergent ***proteorhodopsins*** is stratified according to depth. Here, we present evidence that such photochem. diversity was tuned by Darwinian selection. By using a Bayesian method, we identified sites targeted by Darwinian selection and mapped them to three-dimensional models of ***proteorhodopsins*** . We suggest that spectral fine-tuning results from the combined effect of amino acids that directly interact with retinal and those that influence the confirmation of the retinal-binding pocket.
ST Darwinian adaptation Bacteria ***proteorhodopsin*** light marine environment
IT Statistical analysis
(Bayesian method; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Light
Marine bacteria
(Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Genetic selection
(Darwinian; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Environment
(marine; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Evolution
(mol.; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Conformation
(protein, of retinal-binding pocket; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Rhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsins*** ; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
IT Protein motifs
(retinal-binding pocket, conformation; Darwinian adaptation of ***proteorhodopsin*** to different light intensities in marine environment)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN 2004:791603 CAPLUS <<LOGINID::20060726>>
DN 142:130579
ED Entered STN: 29 Sep 2004
TI Different SAR86 subgroups harbour divergent ***proteorhodopsins***
AU Sabehl, Gazalah; Beja, Oded; Suzuki, Marcelino T.; Preston, Christina M.; DeLong, Edward F.
CS Department of Biology, Technion-Israel Institute of Technology, Haifa, 32000, Israel
SO Environmental Microbiology (2004), 6(9), 903-910
CODEN: ENMIFM; ISSN: 1462-2912
PB Blackwell Publishing Ltd.
DT Journal
LA English
CC 10-4 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 3, 6
AB ***Proteorhodopsins*** (PRs), bacterial photoactive proton pumps, were originally detected in the uncultured marine .gamma.-proteobacterial SAR86 group. PRs are now known to occur in both the .gamma. and .alpha. marine proteobacterial lineages. Recent environmental shotgun sequence anal. in the Sargasso Sea has added yet more diversity, and a potentially broader taxonomic distribution, to the PR family. Much remains to be learned, however, about within-taxon PR variability and the broader organismal distribution of different PR types. We report here genomic analyses of large genome fragments from different subgroups of the SAR86 lineage, recovered from naturally occurring bacterioplankton populations in coastal Red Sea and open ocean Pacific waters. Sequence comparisons were performed on large bacterial artificial chromosomes (BACs) bearing both rRNA and PR genes, derived from different SAR86 subgroups. Our analyses indicated the presence of different PR sequence types within the same SAR86 rRNA subgroup. The data suggested that the distribution of particular PR types does not necessarily parallel the phylogenetic relationship inferred from highly conserved genes such as rRNA. Further analyses of the genomic regions flanking PR also revealed a potential pathway for the biosynthesis of retinal, the PR chromophore that is required to generate the functionally active photoprotein. Finally, comparison of our results with recently reported Sargasso Sea environmental shotgun sequence assemblies demonstrated the utility of BAC clones for interpreting environmental shotgun sequence data, much of which is represented in short contigs that have an overall low depth of coverage.
ST sequence protein DNA ***proteorhodopsin*** proteobacterium rDNA phylogeny
IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S, genes for, phylogeny; phylogenetic anal. of ***proteorhodopsins*** and rDNA from marine .gamma. proteobacteria SAR86 subgroups)
IT Seawater
(Pacific, proteobacteria from; phylogenetic anal. of ***proteorhodopsins*** and rDNA from marine .gamma. proteobacteria SAR86 subgroups)

IT Coastal waters
(Red Sea, proteobacteria from; phylogenetic anal. of
· ***proteorhodopsins*** and rDNA from marine .gamma. proteobacteria
SAR86 subgroups)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(eBACHOT4E07.01 - eBACHOT4E07.66 and Red20E09-01 - Red20E09-148;
phylogenetic anal. of ***proteorhodopsins*** and rDNA from marine
.gamma. proteobacteria SAR86 subgroups)
IT Proteobacteria
(gamma group, subgroup SAR86-I; phylogenetic anal. of
proteorhodopsins and rDNA from marine .gamma. proteobacteria
SAR86 subgroups)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(genes eBACHOT4E07.01 - eBACHOT4E07.66, and Red20E09-01 - Red20E09-148;
phylogenetic anal. of ***proteorhodopsins*** and rDNA from marine
.gamma. proteobacteria SAR86 subgroups)
IT Evolution
(mol.; phylogenetic anal. of ***proteorhodopsins*** and rDNA from
marine .gamma. proteobacteria SAR86 subgroups)
IT DNA sequences
Protein sequences
(phylogenetic anal. of ***proteorhodopsins*** and rDNA from marine
.gamma. proteobacteria SAR86 subgroups)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(***proteorhodopsins*** ; phylogenetic anal. of
proteorhodopsins and rDNA from marine .gamma. proteobacteria
SAR86 subgroups)
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        (amino acid sequence; phylogenetic anal. of   ***proteorhodopsins***
        and rDNA from marine .gamma. proteobacteria SAR86 subgroups)
IT   668960-21-2   689191-23-9
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (nucleotide sequence; phylogenetic anal. of   ***proteorhodopsins***
        and rDNA from marine .gamma. proteobacteria SAR86 subgroups)
RE.CNT  25    THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L1   ANSWER 22 OF 45  CAPLUS  COPYRIGHT 2006 ACS on STN
AN   2004:610146  CAPLUS &lt;&lt;LOGINID::20060726&gt;&gt;
DN   141:135980
ED   Entered STN:  30 Jul 2004
TI     ***Proteorhodopsin***   mutants with improved optical characteristics
IN   Jensen, Rasmus B.; Kelemen, Bradley R.
PA   Genencor International, Inc., USA; Dow Corning Corporation
SO   PCT Int. Appl., 316 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
IC   ICM  C12N
CC   6-3 (General Biochemistry)
     Section cross-reference(s): 3
FAN.CNT 2
     PATENT NO.          KIND   DATE        APPLICATION NO.         DATE
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PI   WO 2004063326        A2    20040729    WO 2003-US38194         20031126
     WO 2004063326        A3    20060216
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
             LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO,
             NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ,
             TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,
             BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,
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             TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
     CA 2506987           AA    20040729    CA 2003-2506987         20031126
     AU 2003302734        A1    20040810    AU 2003-302734          20031126
     US 2005095605        A1    20050505    US 2003-724264          20031126
     EP 1576144           A2    20050921    EP 2003-811664          20031126
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     JP 2006516389        T2    20060706    JP 2004-566503        20031126
PRAI US 2002-429518P      P     20021126
     WO 2003-US38194      W     20031126
CLASS
 PATENT NO.      CLASS  PATENT FAMILY CLASSIFICATION CODES
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 WO 2004063326   ICM    C12N
                 IPCI   C12N [ICM,7]; C07K0014-195 [ICS,7]; C07H0021-04
                        [ICS,7]; C07H0021-00 [ICS,7,C*]; C12P0021-06 [ICS,7]
                 IPCR   C07H0021-00 [I,C*]; C07K0014-435 [I,C*]; C12Q0001-68
                        [I,C*]; C07H0021-04 [I,A]; C07K0014-705 [I,A];
                        C12Q0001-68 [I,A]
                 ECLA   C07H021/04; C07K014/705
 CA 2506987      IPCI   C12N0015-31 [ICM,7]; C12N0015-09 [ICS,7]; C07K0001-107
                        [ICS,7]; C07K0001-00 [ICS,7,C*]; C07K0014-195 [ICS,7]
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 AU 2003302734   IPCI   C12N [ICM,7]
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 US 2005095605   IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00
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                        [ICS,7,C*]
                 IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435
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                        C12Q0001-68 [I,C*]
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                        C12Q0001-68 [I,C*]
                 ECLA   C07H021/04; C07K014/705
 JP 2006516389   IPCI   C12N0015-09 [I,A]; C12P0021-02 [I,A]; C07K0014-195
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                 FTERM  4B024/AA03; 4B024/AA11; 4B024/BA80; 4B024/CA04;
                        4B024/DA05; 4B024/EA04; 4B024/GA11; 4B024/GA25;
                        4B024/HA01; 4B024/HA03; 4B024/HA11; 4B064/AG01;
                        4B064/CA02; 4B064/CA19; 4B064/CC24; 4B064/DA13;
                        4H045/AA10; 4H045/AA20; 4H045/AA30; 4H045/BA10;
                        4H045/CA11; 4H045/DA50; 4H045/EA50; 4H045/FA72;
                        4H045/FA74
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AB The present invention is directed to a ***proteorhodopsin*** mutant having improved optical characteristics. One improved optical characteristic is having a lower pH(pKrh) at which equal concns. of the acidic and basic spectral form of the ***proteorhodopsin*** mols. are present. Another improved optical characteristic is having a smaller difference in max. absorption wavelength between the basic and the acidic form. The mutant comprises a mutation in a conserved amino acid residue of a ***proteorhodopsin*** variant, which causes spectral shifts. A preferred mutation site is a conserved histidine residue at amino acid position 75 of Bac31A8, or position 77 of Hot75m1, or its equiv. position of a ***proteorhodopsin*** variant. Another preferred mutation site is a conserved arginine residue at amino acid position 94 of Bac31A8, or position 96 of Hot75m1, or its equiv. position of a ***proteorhodopsin*** variant.

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ST     ***proteorhodopsin***   mutant optical property sequence
IT   DNA sequences
     Marine bacteria
     Optical memory devices
     Photoinduced energy transfer
     Protein engineering
     Protein sequences
     UV and visible spectra
        ( ***proteorhodopsin***   mutants with improved optical
        characteristics)
IT   Rhodopsins
     RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified);
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PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***proteorhodopsins*** ; ***proteorhodopsin*** mutants with improved optical characteristics)

IT Transport proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proton pump; ***proteorhodopsin*** mutants with improved optical characteristics)

IT Biological transport
(proton pumping; ***proteorhodopsin*** mutants with improved optical characteristics)

IT Mutagenesis
(site-directed; ***proteorhodopsin*** mutants with improved optical characteristics)

IT 727436-82-0P 727436-84-2P 727436-86-4P 727436-87-5P 727436-89-7P
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RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified);
PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; ***proteorhodopsin*** mutants with improved optical characteristics)

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RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified);
PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; ***proteorhodopsin*** mutants with improved optical characteristics)

IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(pumping of; ***proteorhodopsin*** mutants with improved optical characteristics)
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RL: PRP (Properties)
(unclaimed nucleotide sequence; ***proteorhodopsin*** mutants with improved optical characteristics)

L1 ANSWER 23 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:506894 CAPLUS <<LOGINID::20060726>>
DN 141:186511
ED Entered STN: 24 Jun 2004
TI Structural Changes in the Photoactive Site of ***Proteorhodopsin*** during the Primary Photoreaction
AU Bergo, Vladislav; Amsden, Jason J.; Spudich, Elena N.; Spudich, John L.; Rothschild, Kenneth J.
CS Department of Physics, Molecular Biophysics Laboratory, Boston University, Boston, MA, 02215, USA
SO Biochemistry (2004), 43(28), 9075-9083
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
CC 6-1 (General Biochemistry)
AB ***Proteorhodopsin*** (PR), found in marine .gamma.-proteobacteria, is a newly discovered light-driven proton pump similar to bacteriorhodopsin (BR). Because of the widespread distribution of proteobacteria in the worldwide oceanic waters, this pigment may contribute significantly to the global solar energy input in the biosphere. The authors examd. structural changes that occur during the primary photoreaction (PR .fwdarw. K) of wild-type pigment and two mutants using low-temp. FTIR difference spectroscopy. Several vibrations detected in the 3500-3700 cm-1 region are assigned on the basis of H2O .fwdarw. H218O exchange to the perturbation of one or more internal water mols. Substitution of the neg. charged Schiff base counterion, Asp-97, with the neutral asparagine caused a downshift of the ethylenic (C = C) and Schiff base (C = N) stretching modes, in agreement with the 27 nm red shift of the visible .lambda.max. However, this replacement did not alter the normal all-trans to 13-cis isomerization of the chromophore or the environment of the detected water mol.(s). In contrast, substitution of Asn-230, which is in a position to interact with the Schiff base, with Ala induces a 5 nm red shift of the visible .lambda.max and alters the PR chromophore structure, its isomerization to K, and the environment of the detected internal water mols. The combination of FTIR and site-directed mutagenesis establishes that both Asp-97 and Asn-230 are perturbed during the primary phototransition. The environment of Asn-230 is further altered during the thermal decay of K. These results suggest that significant differences exist in the conformational changes which occur in the photoactive sites of ***proteorhodopsin*** and bacteriorhodopsin during the primary photoreaction.
ST ***proteorhodopsin*** photoactive site Asn Asp photoreaction
IT Isomerization
(cis-trans, photochem.; photoinduced perturbation of Asp-97 and Asn-230 in photoactive site of ***proteorhodopsin***)
IT Proteobacteria
(gamma group; photoinduced perturbation of Asp-97 and Asn-230 in photoactive site of ***proteorhodopsin***)
IT Photochemistry
(photoinduced perturbation of Asp-97 and Asn-230 in photoactive site of ***proteorhodopsin***)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); BIOL (Biological study); PROC (Process)
(***proteorhodopsins*** ; photoinduced perturbation of Asp-97 and Asn-230 in photoactive site of ***proteorhodopsin***)

IT   56-84-8, L-Aspartic Acid, biological studies   70-47-3, L-Asparagine, biological studies
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); BIOL (Biological study); PROC (Process)
(photoinduced perturbation of Asp-97 and Asn-230 in photoactive site of ***proteorhodopsin***)

RE.CNT 54   THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1   ANSWER 24 OF 45 CAPLUS

AN   2004:467948 CAPLUS <<LOGINID::20060726>>

DN   141:25187

ED   Entered STN: 10 Jun 2004

TI   Optical information carrier comprising immobilized ***proteorhodopsin*** , security ink, and preparation

IN   Jensen, Rasmus B.; Kelemen, Bradley R.; McAuliffe, Joseph C.; Smith, Wyatt C.

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PA   Genencor International, Inc., USA; Dow Corning Corporation
SO   PCT Int. Appl., 37 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
IC   ICM  C08K
CC   42-12 (Coatings, Inks, and Related Products)
     Section cross-reference(s): 74
FAN.CNT 2
     PATENT NO.           KIND   DATE       APPLICATION NO.        DATE
     ---------------      ----   --------   --------------------   --------
PI   WO 2004048451         A2    20040610   WO 2003-US38157        20031126
     WO 2004048451         A3    20060216
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
             LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO,
             NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ,
             TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,
             BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,
             ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK,
             TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
     CA 2507165            AA    20040610   CA 2003-2507165        20031126
     AU 2003298777         A1    20040618   AU 2003-298777         20031126
     US 2005095605         A1    20050505   US 2003-724264         20031126
     EP 1576042            A2    20050921   EP 2003-796535         20031126
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
     JP 2006515683         T2    20060601   JP 2004-555825         20031126
PRAI US 2002-429518P       P     20021126
     WO 2003-US38157       W     20031126
CLASS
 PATENT NO.      CLASS  PATENT FAMILY CLASSIFICATION CODES
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 WO 2004048451   ICM    C08K
                 IPCI   C08K [ICM,7]; C07K0014-195 [ICS,7]; B29D0017-00
                        [ICS,7]; C09D0011-04 [ICS,7]
                 IPCR   C07H0021-00 [I,C*]; C07K0014-435 [I,C*]; C12Q0001-68
                        [I,C*]; C07H0021-04 [I,A]; C07K0014-705 [I,A];
                        C12Q0001-68 [I,A]
                 ECLA   C07H021/04
 CA 2507165      IPCI   C07K0017-04 [ICM,7]; C07K0017-00 [ICM,7,C*];
                        G11B0007-0045 [ICS,7]; G11B0007-00 [ICS,7,C*];
                        C09D0011-04 [ICS,7]; G11B0007-24 [ICS,7]; G11B0007-26
                        [ICS,7]
                 IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435
                        [I,C*]; C07K0014-705 [I,A]; C12Q0001-68 [I,A];
                        C12Q0001-68 [I,C*]
                 ECLA   C07H021/04
 AU 2003298777   IPCI   C08K [ICM,7]
                 IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435
                        [I,C*]; C07K0014-705 [I,A]; C12Q0001-68 [I,A];
                        C12Q0001-68 [I,C*]
 US 2005095605   IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00
                        [ICS,7,C*]; C07K0014-705 [ICS,7]; C07K0014-435
                        [ICS,7,C*]
                 IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435
                        [I,C*]; C07K0014-705 [I,A]; C12Q0001-68 [I,A];
                        C12Q0001-68 [I,C*]
                 NCL    435/006.000
 EP 1576042      IPCI   C08K0003-00 [ICM,7]
                 IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-435
                        [I,C*]; C07K0014-705 [I,A]; C12Q0001-68 [I,A];
                        C12Q0001-68 [I,C*]
                 ECLA   C07H021/04
 JP 2006515683   IPCI   G03C0001-73 [I,A]; B42D0015-10 [I,A]
                 FTERM  2C005/HA02; 2C005/HB01; 2C005/HB10; 2C005/JB11;
                        2H123/AA00; 2H123/AA01; 2H123/BA00; 2H123/BA13;
                        2H123/CA00; 2H123/CA32
AB   The materials comprise hydrophilic polymers and immobilized
       ***proteorhodopsin***  .  The material comprises .gtoreq.1 hydrophilic
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polymers that form a homogeneous phase with ***proteorhodopsin*** prior to solidification to a solid form. The hydrophilic polymer may be SiO2 sol-gel, gelatin, poly(vinyl alc.), agarose, agar, Me cellulose, polyvinyl acetate, polyvinyl pyrrolidone, polyethylene glycol, or a mixt. The solid material having immobilized ***proteorhodopsin*** is deposited on a substrate selected from glass, paper, metal, fabric material, plastic material, and used as an optical data storage material or a fraud-proof carrier. A security ink may also comprise ***proteorhodopsin*** and .gtoreq.1 hydrophilic polymers.

ST optical film hydrophilic polymer immobilized ***proteorhodopsin*** holog property; security ink photochromatic ***proteorhodopsin*** immobilized; information storage immobilized ***proteorhodopsin***

IT Inks
(marking, photochromatic; optical information carrier comprising hydrophilic polymer-immobilized ***proteorhodopsin*** in coating or ink layer that is difficult to copy)

IT Coating materials
Optical memory devices
(optical information carrier comprising hydrophilic polymer-immobilized ***proteorhodopsin*** in coating or ink layer that is difficult to copy)

IT Gelatins, uses
Polyoxyalkylenes, uses
Silica gel, uses
RL: TEM (Technical or engineered material use); USES (Uses)
(optical information carrier comprising hydrophilic polymer-immobilized ***proteorhodopsin*** in coating or ink layer that is difficult to copy)

IT Proteins
Rhodopsins
RL: TEM (Technical or engineered material use); USES (Uses)
(***proteorhodopsin*** ; optical information carrier comprising hydrophilic polymer-immobilized ***proteorhodopsin*** in coating or ink layer that is difficult to copy)

IT 9000-01-5, Arabic gum 9002-18-0, Agar 9002-89-5, Poly(vinyl alcohol) 9003-20-7, Polyvinyl acetate 9003-39-8, Polyvinyl pyrrolidone 9004-67-5, Methyl cellulose 9012-36-6, Agarose 25322-68-3, Polyethylene glycol 58059-65-7, Acrylamide-bisacrylamide copolymer
RL: TEM (Technical or engineered material use); USES (Uses)
(optical information carrier comprising hydrophilic polymer-immobilized ***proteorhodopsin*** in coating or ink layer that is difficult to copy)

IT 78-10-4, Tetraethylorthosilicate
RL: TEM (Technical or engineered material use); USES (Uses)
(sol-gel; optical information carrier comprising hydrophilic polymer-immobilized ***proteorhodopsin*** in coating or ink layer that is difficult to copy)

L1 ANSWER 25 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:444244 CAPLUS <<LOGINID::20060726>>
DN 141:203173
ED Entered STN: 02 Jun 2004
TI Light-induced intramolecular charge movements in microbial rhodopsins in intact E. coli cells
AU Sineshchekov, Oleg A.; Spudich, John L.
CS Center for Membrane Biology, Department of Biochemistry and Molecular Biology and Department of Microbiology and Molecular Genetics, University of Texas Medical School, Houston, TX, 77030, USA
SO Photochemical & Photobiological Sciences (2004), 3(6), 548-554
CODEN: PPSHCB; ISSN: 1474-905X
PB Royal Society of Chemistry
DT Journal
LA English
CC 10-6 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 9
AB Microbial rhodopsins undergo cyclic photochem. reactions (photocycles) in which proton transfers and conformational changes result in charge displacements during transitions between photocycle intermediates. We report a new photoelec. method to monitor charge movements during rhodopsin photocycling with fast kinetic resoln. in suspensions of intact Escherichia coli cells. The method monitors elec. currents resulting from asym. photoexcitation of microbial rhodopsins by a unilateral laser flash,

and kinetically resolves intramol. charge movements. We investigated E. coli-expressed proton-transporting rhodopsins, specifically green- and blue-absorbing ***proteorhodopsins*** (GPR and BPR, resp.) from uncultivated marine plankton, and sensory rhodopsins, namely receptors from Natronomonas pharaonis and Anabaena (Nostoc) sp. PCC7120. Kinetic components of the currents correlate with photochem. transformations of the pigments, and the integrated current measures net transport by the proton-pumping rhodopsins. The photoelec. measurements distinguish between known light-driven transporters and photosensors, and reveal differences in proton transfer reactions in the 2 tested proton pumps. Screening of 9 newly identified ***proteorhodopsins*** reveals 2 with GPR-type charge movements, 5 with BPR-type, and 2 with the characteristics of the sensory rhodopsins. The approach developed in the present work provides a direct, rapid and informative method for studying electrogenic events in rhodopsin photocycles and also gives a clue to functions of newly found microbial rhodopsins in nature.

ST photoelec detn photocycle rhodopsin Escherichia

IT Escherichia coli
Light
Photoemission
Photolysis
(light-induced intramol. charge movements in microbial rhodopsins in intact Escherichia coli cells)

IT Rhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsins*** ; light-induced intramol. charge movements in microbial rhodopsins in intact Escherichia coli cells)

RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 26 OF 45 CAPLUS

AN 2004:354194 CAPLUS <<LOGINID::20060726>>

DN 141:256078

ED Entered STN: 30 Apr 2004

TI Characterization of RS29, a blue-green ***proteorhodopsin*** variant from the Red Sea

AU Man-Aharonovich, Dikla; Sabehi, Gazalah; Sineshchekov, Oleg A.; Spudich,

Elena N.; Spudich, John L.; Beja, Oded
CS Department of Biology, Technion-Israel Institute of Technology, Haifa, 32000, Israel
SO Photochemical & Photobiological Sciences (2004), 3(5), 459-462
CODEN: PPSHCB; ISSN: 1474-905X
PB Royal Society of Chemistry
DT Journal
LA English
CC 6-3 (General Biochemistry)
Section cross-reference(s): 3, 10
AB Using structural modeling comparisons and mutagenesis, amino acid residue 105 was found to function as a spectral tuning switch in marine ***proteorhodopsins*** (PR). Changes at this position account for most of the spectral difference between blue-absorbing PRs (B-PRs), and green-absorbing PRs (G-PRs). Here we analyzed a Red Sea variant (RS29) from a new family of PRs that is composed of G-PR type variants that possess glutamine instead of leucine at position 105 like in B-PRs. The absorption spectrum as well as photocycle of RS29 variant were measured and compared to point-mutated 'position 105' PRs. Unexpectedly, the absorption max. of RS29 was 515 nm, a smaller blue shift compared to the 498 nm max. of G-PR_L105Q. We found that two addnl. residues at positions 65 and 70 each contribute a small red shift to the absorption spectrum of G-PR and therefore appear to account for the intermediate absorption max. of RS29 by their opposing influences on the spectrum. Our results show that in addn. to the retinal pocket position 105 determinant, other residues predicted to be outside the retinal pocket fine-tune the absorption spectra of marine PRs. The RS29 photochem. reaction cycle was found to be 2 orders of magnitude slower than that of G-PR with a t1/2 of >600 ms. This result raises the possibility of regulatory (i.e. sensory) rather than energy harvesting functions for some members of the PR family.
ST rhodopsin ***proteorhodopsin*** sequence variant RS29 Red Sea bacteria
IT Biological transport
Eubacteria
(characterization of RS29 blue-green ***proteorhodopsin*** variant from the Red Sea)
IT DNA sequences
Protein sequences
(characterization of RS29, a blue-green ***proteorhodopsin*** variant from the Red Sea)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; characterization of RS29 blue-green ***proteorhodopsin*** variant from the Red Sea)
IT 681705-41-9 681705-43-1 681705-45-3
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; characterization of RS29, a blue-green ***proteorhodopsin*** variant from the Red Sea)
IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(characterization of RS29 blue-green ***proteorhodopsin*** variant from the Red Sea)
IT 681705-40-8 681705-42-0 681705-44-2
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; characterization of RS29, a blue-green ***proteorhodopsin*** variant from the Red Sea)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 27 OF 45 CAPLUS
AN 2004:340181 CAPLUS <<LOGINID::20060726>>
DN 141:85231
ED Entered STN: 27 Apr 2004
TI Search for the retinal-type photosynthetic microorganisms from the Japanese Sea
AU Ihara, Kunio; Sugiura, Kana; Ito, Shigeru
CS Center for Gene Research, Nagoya University, Chikusa-ku, Nagoya, 464-8602, Japan
SO Kankyo Kagaku Sogo Kenkyusho Nenpo (2003), Volume Date 2002, 22, 51-60
CODEN: KASND6; ISSN: 0285-5895
PB Kankyo Kagaku Sogo Kenkyusho
DT Journal
LA English
CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 3, 6
AB Sunlight takes an important role in our sustenance: all the food we eat and all the fossil fuel we use is a product of photosynthesis, which is the process that converts light energy to chem. energy that can be used by many organisms contg. us. Photosynthesis is carried out by many different organisms, ranging from higher green plants to basic bacteria. A major part of photosynthesis occurred in oceans. Until recently, all photosynthetic organisms are considered to use a chlorophyll (or bacteriochlorophyll) as light energy capturing chromophore with an exception of photosynthetic archaea Halobacteria, which can produce ATP (ATP) using a retinal protein, called bacteriorhodopsin, in the light. At the last year of 20th century, uncultured .gamma.-proteobacteria, which was estd. to occupy as much as 10 percent of surface seawater in some places, were found to harbor the novel light driven proton pump, ***proteorhodopsin*** , through the environmental genomics study. Thus, we tried to isolate a similar ***proteorhodopsin*** gene using PCR method from the Japanese sea and successfully confirmed the existence of retinal-based microorganism in the Japanese Sea. From sequence comparisons among archaeal type rhodopsin families, its phylogenetic position was discussed. Finally, a trial to select the retinal-based photosynthetic bacteria using this partial gene fragment was described.
ST ***proteorhodopsin*** sequence marine photosynthetic microorganism Japanese Sea
IT Evolution
(mol., of ***proteorhodopsin*** ; from retinal-type photosynthetic microorganisms from Japanese Sea)
IT Protein sequences
(of ***proteorhodopsin*** ; of retinal-type photosynthetic microorganisms from Japanese Sea)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(proteo-; retinal-type photosynthetic microorganisms from Japanese Sea)
IT Marine microorganism
Seawater
(retinal-type photosynthetic microorganisms from Japanese Sea)
IT 714396-79-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; retinal-type photosynthetic microorganisms from Japanese Sea)
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN 2004:126417 CAPLUS <<LOGINID::20060726>>
DN 140:370377
ED Entered STN: 17 Feb 2004
TI The influence of water on the photochemical reaction cycle of ***proteorhodopsin*** at low and high pH
AU Lakatos, Melinda; Varo, Gyorgy
CS Institute of Biophysics, Biological Research Center, Hungarian Academy of Sciences, Szeged, H-6701, Hung.
SO Journal of Photochemistry and Photobiology, B: Biology (2004), 73(3), 177-182
CODEN: JPPBEG; ISSN: 1011-1344
PB Elsevier Science B.V.
DT Journal
LA English
CC 6-3 (General Biochemistry)
AB Dried samples were prepd. from suspension of ***proteorhodopsin*** . With HCl and NaOH the pH of the samples was adjusted below and above the pKa of the proton acceptor Asp-97, which was established earlier to be 7.1. Both types of samples were photoactive, and exhibited a truncated photocycle, compared to that measured in suspension. The photocycle of the low pH sample had a K like red shifted intermediate, decaying through an energized PR' intermediate to the ground state protein. The high pH sample had a more complex photocycle in which beside of the red shifted intermediate an M like intermediate could be identified, having a deprotonated Schiff-base. This blue shifted intermediate decays through an intermediate, we designated PR', which is spectrally identical to the unphotolyzed ground state. The humidity and temp. dependence of the photocycle in both cases was studied to understand the role of water in the function of the ***proteorhodopsin*** . The effects measured on ***proteorhodopsin*** were very similar to that measured earlier on bacteriorhodopsin.
ST water photocycle bacteriorhodopsin ***proteorhodopsin*** proton transport pH temp
IT Biological transport
(hydrogen ion; influence of water on photochem. reaction cycle of ***proteorhodopsin*** at low and high pH)
IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(influence of water on photochem. reaction cycle of ***proteorhodopsin*** at low and high pH)
IT 7732-18-5, Water, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(influence of water on photochem. reaction cycle of ***proteorhodopsin*** at low and high pH)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L1 ANSWER 29 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:59797 CAPLUS <<LOGINID::20060726>>
DN 140:266392
ED Entered STN: 26 Jan 2004
TI Selectivity of Retinal Photoisomerization in ***Proteorhodopsins*** Is Controlled by Aspartic Acid 227
AU Imasheva, Eleonora S.; Balashov, Sergei P.; Wang, Jennifer M.; Dioumaev, Andrei K.; Lanyi, Janos K.
CS Department of Physiology and Biophysics, University of California, Irvine, CA, 92697, USA
SO Biochemistry (2004), 43(6), 1648-1655
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
CC 6-3 (General Biochemistry)
AB Similarly to bacteriorhodopsin, ***proteorhodopsin*** that normally contains all-trans and 13-cis retinal is transformed at low pH to a species contg. 9-cis retinal under continuous illumination at .lambda. > 530 nm. This species, absorbing around 430 nm, returns thermally in tens of minutes to initial pigment and can be reconverted also with blue-light illumination. The yield of the 9-cis species is negligibly small at neutral pH but increases manyfold (>100) at acid pH with a pKa of 2.6. This indicates that protonation of acidic group(s) alters the photoreaction pathway that leads normally to all-trans .fwdarw. 13-cis isomerization. In the D97N mutant, in which one of the two acidic groups in the vicinity of the retinal Schiff base is not ionizable, the yield of 9-cis species at low pH shows a pH dependence similar to that in the wild-type but with a somewhat increased pKa of 3.3. In contrast to this relatively minor effect, replacement of the other acidic group, Asp227, with Asn results in a remarkable, more than 50-fold, increase in the yield of the light-induced formation of 9-cis species in the pH range 4-6. It appears that protonation of Asp227 at low pH is what causes the dramatic increase in the yield of the 9-cis species in wild-type ***proteorhodopsin*** . We conclude that the photoisomerization pathways in ***proteorhodopsin*** to 13-cis or 9-cis photoproducts are controlled by the charge state of Asp227.
ST retina retinal photoisomerization ***proteorhodopsin*** aspartic acid protonation
IT Protonation
(Asp227 residue of ***proteorhodopsin*** is crit. of retinal photoisomerization and enhances 9-cis retinal photoproduct at acidic pH)
IT Schiff bases
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Asp227 residue of ***proteorhodopsin*** is crit. of retinal photoisomerization and enhances 9-cis retinal photoproduct at acidic pH)
IT Isomerization
(photoisomerization; Asp227 residue of ***proteorhodopsin*** is crit. of retinal photoisomerization and enhances 9-cis retinal photoproduct at acidic pH)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsin*** ; Asp227 residue of ***proteorhodopsin*** is crit. of retinal photoisomerization and enhances 9-cis retinal photoproduct at acidic pH)
IT 56-84-8, Aspartic acid, biological studies 116-31-4, all-trans-Retinal

472-86-6, 13-cis-Retinal   514-85-2, 9-Cis-Retinal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Asp227 residue of   ***proteorhodopsin***   is crit. of retinal photoisomerization and enhances 9-cis retinal photoproduct at acidic pH)

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L1   ANSWER 30 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN   2003:923788 CAPLUS <<LOGINID::20060726>>
DN   140:89566
ED   Entered STN: 26 Nov 2003
TI   ***Proteorhodopsin***   in living color: diversity of spectral properties within living bacterial cells
AU   Kelemen, Bradley R.; Du, Mai; Jensen, Rasmus B.
CS   Genencor International, Inc., Palo Alto, CA, 94304, USA
SO   Biochimica et Biophysica Acta, Biomembranes (2003), 1618(1), 25-32
     CODEN: BBBMBS; ISSN: 0005-2736
PB   Elsevier B.V.
DT   Journal
LA   English
CC   6-3 (General Biochemistry)
     Section cross-reference(s): 10
AB   ***Proteorhodopsin***   is a family of over 50 proteins that provide phototrophic capability to marine bacteria by acting as light-powered proton pumps. The potential importance of   ***proteorhodopsin***   to

global ocean ecosystems and the possible applications of ***proteorhodopsin*** in optical data storage and optical signal processing have spurred diverse research in this new family of proteins. We show that ***proteorhodopsin*** expressed in Escherichia coli is functional and properly inserted in the membrane. At high expression levels, it appears to self-assoc. We present a method for detg. spectral properties of ***proteorhodopsin*** in intact E. coli cells that matches results obtained with detergent-solubilized, purified proteins. Using this method, we observe distinctly different spectra for protonated and deprotonated forms of 21 natural ***proteorhodopsin*** proteins in intact E. coli cells. Upon protonation, the wavelength maxima red shifts between 13 and 53 nm. We find that pKa values between 7.1 and 8.5 describe the pH-dependent spectral shift for all of the 21 natural variants of ***proteorhodopsin*** . The wavelength maxima of the deprotonated forms of the 21 natural ***proteorhodopsins*** cluster in two sequence-related groups: blue ***proteorhodopsins*** (B-PR) and green ***proteorhodopsins*** (G-PR). The site-directed substitution Leu105Gln in Bac31A8 ***proteorhodopsin*** shifts this G-PR's wavelength max. to the same wavelength max. as that of the B-PR Hot75m1 ***proteorhodopsin*** . The site-directed substitution Gln107Leu in Hot75m1 ***proteorhodopsin*** shifts this B-PR's wavelength max. to the same wavelength max. as that of Bac31A8 ***proteorhodopsin*** .

ST ***proteorhodopsin*** spectra protonation deprotonation Escherichia

IT Self-association
(***proteorhodopsin*** expressed at high levels in E. coli shows evidence of self-assocn.)

IT Deprotonation
Escherichia coli
Protonation
(***proteorhodopsins*** exhibit diverse protonation/deprotonation-assocd. spectral properties in E. coli cells)

IT Rhodopsins
RL: PRP (Properties)
(***proteorhodopsins*** ; ***proteorhodopsins*** exhibit diverse protonation/deprotonation-assocd. spectral properties in E. coli cells)

RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 31 OF 45 CAPLUS

AN 2003:876481 CAPLUS <<LOGINID::20060726>>

DN 140:36866

ED Entered STN: 10 Nov 2003

TI ***Proteorhodopsin*** genes are distributed among divergent marine bacterial taxa

AU de la Torre, Jose R.; Christianson, Lynne M.; Beja, Oded; Suzuki, Marcelino T.; Karl, David M.; Heidelberg, John; DeLong, Edward F.
CS Monterey Bay Aquarium Research Institute, Moss Landing, CA, 95039, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(22), 12830-12835
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 10
AB ***Proteorhodopsin*** (PR) is a retinal-binding bacterial integral membrane protein that functions as a light-driven proton pump. The gene encoding this photoprotein was originally discovered on a large genome fragment derived from an uncultured marine .gamma.-proteobacterium of the SAR86 group. Subsequently, many variants of the PR gene have been detected in marine plankton, via PCR-based gene surveys. It has not been clear, however, whether these different PR genes are widely distributed among different bacterial groups, or whether they have a restricted taxonomic distribution. This report provides comparative analyses of PR-bearing genomic fragments recovered directly from planktonic bacteria inhabiting the California coast, the central Pacific Ocean, and waters offshore the Antarctica Peninsula. Sequence anal. of an Antarctic genome fragment harboring PR (ANT32C12) revealed moderate conservation in gene order and identity, compared with a previously reported PR-contg. genome fragment from a Monterey Bay .gamma.-proteobacterium (EBAC31A08). Outside the limited region of synteny shared between these clones, however, no significant DNA or protein identity was evident. Anal. of a third PR-contg. genome fragment (HOT2C01) from the North Pacific subtropical gyre showed even more divergence from the .gamma.-proteobacterial PR-flanking region. Subsequent phylogenetic and comparative genomic analyses revealed that the Central North Pacific PR-contg. genome fragment (HOT2C01) originated from a planktonic .alpha.-proteobacterium. These data indicate that PR genes are distributed among a variety of divergent marine bacterial taxa, including both .alpha.- and .gamma.-proteobacteria. These analyses also demonstrate the utility of cultivation-independent comparative genomic approaches for assessing gene content and distribution in naturally occurring microbes.
ST ***proteorhodopsin*** gene sequence distribution marine bacteria
IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ABC (ATP-binding cassette) transporters; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(BCCP (biotin carboxyl-carrier protein); ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Translation elongation factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(EF-G; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Translation elongation factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(EF-Tu; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L10; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L11; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(L14; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L16; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L17; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L18; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L1; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L22; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L23; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L24; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L28; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L2; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L3; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L4; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L5; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L6; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(L7/L12; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)

IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(NMN-transporting; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT DNA formation factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(N'; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(OMP (outer membrane protein), TolC; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(PBP (penicillin-binding protein), PBP 6 (penicillin-binding protein 6); ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(PBP 2 (penicillin-binding protein 2); ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(RodA; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S11; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S13; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S14; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S4; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S5; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S7; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S8; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteobacteria
(alpha group; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(cation-transporting; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteobacteria
(gamma group; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene nusG; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Plankton
(marine bacterio-; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Evolution
(mol.; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Plankton
(pico-; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Transport proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(preprotein transporter; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(proteo-; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT DNA sequences
Protein sequences
(***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Flavodoxin
Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Lipoproteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(secreted; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(secretory; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(single-stranded DNA-binding; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(.rho.; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
IT 9012-66-2, 5-Dehydroquinate dehydratase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(II; ***proteorhodopsin*** genes are distributed among divergent marine bacterial taxa)
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence;   ***proteorhodopsin***   genes are distributed
among divergent marine bacterial taxa)

IT   609703-61-9   609703-62-0   609703-63-1   609703-64-2   609703-65-3
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634653-30-8   634653-31-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence;   ***proteorhodopsin***   genes are distributed
among divergent marine bacterial taxa)

IT   288364-64-7   609701-87-3   609702-27-4   609702-69-4   609703-29-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence;   ***proteorhodopsin***   genes are distributed
among divergent marine bacterial taxa)

IT   9001-80-3, 6-Phosphofructokinase   9012-30-0, Acetyltransferase
9012-31-1, Acetyl-CoA synthetase   9012-56-0, Amidohydrolase   9013-18-7
9013-25-6, Acetylmuramoyl-L-alanine amidase   9013-66-5, Glutathione
peroxidase   9013-79-0, Esterase   9014-24-8, RNA polymerase   9023-45-4,
Tyrosyl-tRNA synthetase   9023-67-0, Phosphoribosylaminoimidazolesuccinoca

rboxamide synthetase 9023-83-0, Ribose 5-phosphate isomerase
9023-93-2, Acetyl-CoA carboxylase 9024-32-2, Dihydroxyacid dehydratase
9024-34-4, Threonine dehydratase 9026-30-6, Poly(A) polymerase
9026-67-9, Choline kinase 9026-84-0, Ribokinase 9026-99-7,
Phosphopantetheine adenylyltransferase 9027-13-8, Enoyl-coenzyme A
hydratase 9027-45-6, Acetolactate synthase 9027-65-0, Acyl-CoA
dehydrogenase 9027-81-0, Adenylosuccinate lyase 9028-85-7, Formate
dehydrogenase 9028-86-8, Aldehyde dehydrogenase 9030-66-4, Glycerol
kinase 9030-79-9, 3-Hydroxydecanoyl-acyl carrier protein dehydratase
9031-15-6, Leucyl-tRNA synthetase 9031-98-5, Carboxypeptidase
9032-58-0, Geranylgeranyl pyrophosphate synthase 9032-84-2,
Phosphoribosylformylglycinamidine synthase 9036-37-7, Porphobilinogen
synthase 9037-41-6, Nitroreductase 9050-70-8, Proline dehydrogenase
9068-32-0, Exodeoxyribonuclease 9073-60-3, .beta.-Lactamase 9073-96-5,
Saccharopine dehydrogenase 9074-91-3, Porphobilinogen deaminase
9075-02-9, Ketol-acid reductoisomerase 9075-09-6, UDP-N-acetylmuramyl-L-
alanyl-D-glutamate:2,6-diaminopimelate ligase 9075-54-1, Gene mutT
hydrolase 9075-71-2, Biotin carboxylase 9077-10-5, 3-Oxoacyl-ACP
synthase 37217-33-7, DNA polymerase III 37277-85-3, D-Alanine
aminotransferase 37278-18-5, Phosphomethylpyrimidine kinase
37288-24-7, Exoribonuclease 37289-34-2 37292-90-3, Dioxygenase
37318-64-2 37340-95-7, Biotin-(acetyl-CoA carboxylase) synthetase
39369-30-7, RRNA methylase 51901-16-7, 1-Acylglycerol-3-phosphate
acyltransferase 54249-88-6, Xaa-Pro-dipeptidylaminopeptidase
60440-29-1, DNA repair exonuclease 61229-81-0, Methionine aminopeptidase
61584-55-2, 2-Nitropropane dioxygenase 68518-07-0, Glutamate
semialdehyde aminotransferase 72162-84-6, Prolyl endopeptidase
78206-57-2, Peptide methioninesulfoxide reductase 78783-53-6,
Formamidopyrimidine DNA glycosylase 81669-70-7, Metallopeptidase
95076-93-0, Peptidyl-prolyl cis trans isomerase 99676-37-6,
Succinylornithine aminotransferase 104382-17-4, Carnitine dehydratase
114934-93-9, Isomerase, protein disulfide (monothiol thioredoxin)
117698-12-1, Paraoxonase 130590-51-1, MRNA adenine 6-methyltransferase
144941-31-1, DNA topoisomerase IV 157971-99-8, UDP-3-O-acyl-N-
acetylglucosamine deacetylase 430429-15-5, RRNA pseudouridine synthase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(***proteorhodopsin*** genes are distributed among divergent marine
bacterial taxa)

IT 9031-72-5, Alcohol dehydrogenase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(zinc-dependent; ***proteorhodopsin*** genes are distributed among
divergent marine bacterial taxa)

IT 9027-41-2, Hydrolase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(.alpha./.beta.; ***proteorhodopsin*** genes are distributed among
divergent marine bacterial taxa)

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Methods) Version 4.0b10 2001

L1 ANSWER 32 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:864660 CAPLUS <<LOGINID::20060726>>
DN 140:231091
ED Entered STN: 05 Nov 2003
TI Novel ***proteorhodopsin*** variants from the Mediterranean and Red Seas
AU Sabehi, Gazalah; Massana, Ramon; Bielawski, Joseph P.; Rosenberg, Mira; Delong, Edward F.; Beja, Oded
CS Department of Biology, Technion- Israel Institute of Technology, Haifa, 32000, Israel
SO Environmental Microbiology (2003), 5(10), 842-849
CODEN: ENMIFM; ISSN: 1462-2912
PB Blackwell Publishing Ltd.
DT Journal
LA English
CC 6-3 (General Biochemistry)
Section cross-reference(s): 3, 10
AB ***Proteorhodopsins*** , ubiquitous retinylidene photoactive proton pumps, were recently found in the widespread uncultured SAR86 bacterial group in oceanic surface waters. To survey ***proteorhodopsin*** diversity, new degenerate sets of ***proteorhodopsin*** primers were designed based on a genomic ***proteorhodopsin*** gene sequence originating from an Antarctic fosmid library. New ***proteorhodopsin*** variants were identified in Red Sea samples that were most similar to the original green-light absorbing ***proteorhodopsins*** found in Monterey Bay California. Unlike green-absorbing ***proteorhodopsins*** however, these new variants contained a glutamine residue at position 105, the same site recently shown to control spectral tuning in naturally occurring ***proteorhodopsins*** . Different ***proteorhodopsin*** variants were also found in the Mediterranean Sea. These ***proteorhodopsins*** formed new and distinctive ***proteorhodopsin*** groups. Phylogenetic analyses show that some of the new variants were very different from previously characterized ***proteorhodopsins*** , and formed the deepest branching groups found so far among marine ***proteorhodopsins*** . The existence of these varied ***proteorhodopsin*** sequences suggests that this class of proteins has undergone substantial evolution. These variants could represent functionally divergent paralogous genes, derived from the same or similar species, or orthologous ***proteorhodopsins*** that are distributed amongst divergent planktonic microbial taxa.
ST ***proteorhodopsin*** gene protein sequence phylogeny marine bacteria
IT Evolution
(mol.; phylogenetic anal. of ***proteorhodopsin*** variants from the Mediterranean and Red Seas)
IT DNA sequences
Protein sequences
(phylogenetic anal. of ***proteorhodopsin*** variants from the Mediterranean and Red Seas)
IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; phylogenetic anal. of ***proteorhodopsin*** variants from the Mediterranean and Red Seas)
IT Marine bacteria
(uncultured; phylogenetic anal. of ***proteorhodopsin*** variants from the Mediterranean and Red Seas)
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624313-00-4 624313-01-5 624313-02-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; phylogenetic anal. of ***proteorhodopsin*** variants from the Mediterranean and Red Seas)
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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; phylogenetic anal. of ***proteorhodopsin*** variants from the Mediterranean and Red Seas)

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L1 ANSWER 33 OF 45 CAPLUS

AN 2003:728678 CAPLUS <<LOGINID::20060726>>

DN 140:37480

ED Entered STN: 17 Sep 2003

TI Crossing the borders: archaeal rhodopsins go bacterial

AU Gartner, Wolfgang; Losi, Aba

CS Max-Planck-Institut fur Strahlenchemie, Mulheim an der Ruhr, D-45470, Germany

SO Trends in Microbiology (2003), 11(9), 405-407
CODEN: TRMIEA; ISSN: 0966-842X

PB Elsevier Science Ltd.

DT Journal; General Review

LA English

CC 6-0 (General Biochemistry)
Section cross-reference(s): 10

AB A review. All-trans-retinal based, light-driven ion pumping and light sensing are no longer an exclusive archaeal enterprise after the exciting discovery of archaeal-type rhodopsins in bacteria and eukarya. Following the discovery of proton-pumping rhodopsins in marine bacteria (***proteorhodopsins***), an archaetypal system, consisting of a membrane-intrinsic sensory rhodopsin and a sol. interacting transducer, was recently identified in the cyanobacterium Anabaena. The powerful approach that combines genome digging' and protein expression is rapidly changing our understanding of light responses in lower organisms.

ST review rhodopsin bacteria Archaea
IT Anabaena
  Cyanobacteria
    (archaeal-type rhodopsin in cyanobacteria)
IT Rhodopsins
  RL: BSU (Biological study, unclassified); BIOL (Biological study)
    (***proteorhodopsins*** ; archaeal-type rhodopsin in cyanobacteria)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 34 OF 45 CAPLUS
AN 2003:684886 CAPLUS <<LOGINID::20060726>>
DN 139:303519
ED Entered STN: 02 Sep 2003
TI Spectroscopic and Photochemical Characterization of a Deep Ocean ***Proteorhodopsin***

AU Wang, Wei-Wu; Sineshchekov, Oleg A.; Spudich, Elena N.; Spudich, John L.
CS Department of Biochemistry and Molecular Biology, Center for Membrane Biology, University of Texas Medical School, Houston, TX, 77030, USA

SO Journal of Biological Chemistry (2003), 278(36), 33985-33991
  CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English

CC 6-3 (General Biochemistry)
  Section cross-reference(s): 10

AB A second group of ***proteorhodopsin*** -encoding genes (blue-absorbing ***proteorhodopsin*** , BPR) differing by 20-30% in predicted primary structure from the first-discovered green-absorbing (GPR) group has been detected in picoplankton from Hawaiian deep sea water. Here we compare BPR and GPR absorption spectra, photochem. reactions, and proton transport activity. The photochem. reaction cycle of Hawaiian deep ocean BPR in cells is 10-fold slower than that of GPR with very low accumulation of a deprotonated Schiff base intermediate in cells and exhibits mechanistic differences, some of which are due to its glutamine residue rather than leucine at position 105. In contrast to GPR and other characterized microbial rhodopsins, spectral titrns. of BPR indicate that a second titratable group, in addn. to the retinylidene Schiff base counterion Asp-97, modulates the absorption spectrum near neutral pH. Mutant anal. confirms that Asp-97 and Glu-108 are proton acceptor and proton donor, resp., in retinylidene Schiff base proton transfer reactions during the BPR photocycle as previously shown for GPR, but BPR contains an alternative acceptor evident in its D97N mutant, possibly the same as the second titratable group modulating the absorption spectrum. BPR, similar to GPR, carries out outward light-driven proton transport in Escherichia coli vesicles but with a reduced translocation rate attributable to its slower photocycle. In energized E. coli cells at physiol. pH, the net effect of BPR photocycling is to generate proton currents dominated by a triggered proton influx, rather than efflux as obsd. with GPR-contg. cells. Reversal of the proton current with the K+-ionophore valinomycin supports that the influx is because of voltage-gated channels in the E. coli cell membrane. These observations demonstrate diversity in photochem. and mechanism among ***proteorhodopsins*** . Calcns. of photon fluence rates at different ocean depths show that the difference in photocycle rates between GPR and BPR as well as their different absorption

maxima may be explained as an adaptation to the different light intensities available in their resp. marine environments. Finally, the results raise the possibility of regulatory (i.e. sensory) rather than energy harvesting functions of some members of the ***proteorhodopsin*** family.

ST picoplankton ***proteorhodopsin*** photocycle proton transport photochem

IT Light
Proton transfer
Protonation
UV and visible spectra
(absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT Schiff bases
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); BIOL (Biological study); PROC (Process)
(absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT Biological transport
(channel-mediated, light-driven; absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT Plankton
(pico-; absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT Rhodopsins
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); BIOL (Biological study); PROC (Process)
(***proteorhodopsin*** ; absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT 61-90-5, Leucine, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(-105, photocycle in relation to; absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT 56-86-0, L-Glutamic acid, biological studies
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); BIOL (Biological study); PROC (Process)
(-108, proton donor; absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT 56-84-8, L-Aspartic acid, biological studies
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); BIOL (Biological study); PROC (Process)
(-97, proton acceptor; absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(absorption spectra, photochem. reactions, and proton transport activity of blue-absorbing- and green-absorbing ***proteorhodopsin*** isoforms from deep ocean picoplankton)

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L1 ANSWER 35 OF 45 CAPLUS
AN 2003:519869 CAPLUS <<LOGINID::20060726>>
DN 139:175490
ED Entered STN: 09 Jul 2003
TI Resonance Raman Characterization of ***Proteorhodopsin*** 's Chromophore Environment
AU Krebs, Richard A.; Dunmire, David; Partha, Ranga; Braiman, Mark S.
CS Syracuse University Chemistry Department, Syracuse, NY, 13244-4100, USA
SO Journal of Physical Chemistry B (2003), 107(31), 7877-7883
CODEN: JPCBFK; ISSN: 1520-6106
PB American Chemical Society
DT Journal
LA English
CC 6-3 (General Biochemistry)
AB ***Proteorhodopsin*** (pR) is a bacteriorhodopsin (bR) homolog, recently discovered in oceanic bacterioplankton, which functions as a light-driven proton pump. Resonance Raman spectra of pR excited with 532-nm light indicate that there are two subpopulations of pR within the sample solubilized in octylglucoside detergent and maintained in a light-adapted state in a spinning Raman cell. The subpopulations exhibit two distinct chromophore environments, as evidenced by two sets of split peaks, 1642/1655 cm-1 (corresponding to the Schiff base .upsilon.C:N vibration) and 1244/1252 cm-1 (corresponding to a retinylidene-lysine N-C-H rock). These populations most likely arise either from different post-translational modifications of the heterologously expressed protein or from a mixt. of retinal isomers (all-trans and 13-cis) that was previously reported to be present in light-adapted pR in a 60:40 ratio. However, the latter possibility seems at odds with the resonance Raman fingerprint spectral patterns in both natural-abundance and 15-2H-retinal-substituted pR, which are consistent with an all-trans chromophore configuration similar to that of light-adapted bR.
ST ***proteorhodopsin*** Schiff base retinal posttranslational processing proton transfer
IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsin*** ; role of posttranslational processing and retinal isomers in two subpopulations of ***proteorhodopsin*** 's chromophore)
IT Hydrogen bond
Post-translational processing
Proton transfer
(role of posttranslational processing and retinal isomers in two subpopulations of ***proteorhodopsin*** 's chromophore)
IT Schiff bases
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(role of posttranslational processing and retinal isomers in two subpopulations of ***proteorhodopsin*** 's chromophore)
IT 116-31-4, all-trans-Retinal 52918-36-2, cis-Retinal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(role of posttranslational processing and retinal isomers in two subpopulations of ***proteorhodopsin*** 's chromophore)
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L1   ANSWER 36 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN   2003:395093 CAPLUS <<LOGINID::20060726>>
DN   139:161209
ED   Entered STN: 23 May 2003
TI   The photochemical reaction cycle of ***proteorhodopsin*** at low pH
AU   Lakatos, Melinda; Lanyi, Janos K.; Szakacs, Julianna; Varo, Gyorgy
CS   Institute of Biophysics, Biological Research Center of the Hungarian Academy of Sciences, Szeged, H-6701, Hung.
SO   Biophysical Journal (2003), 84(5), 3252-3256
CODEN: BIOJAU; ISSN: 0006-3495
PB   Biophysical Society
DT   Journal
LA   English
CC   6-3 (General Biochemistry)
AB   The proton acceptor group in the recently described retinal protein, ***proteorhodopsin*** has an unusually high pKa of 7.1. It was shown that at pH above this pKa, illumination initiates a photocycle similar to that of bacteriorhodopsin, and the protein transports proton across the cell membrane. Recently it was reported that ***proteorhodopsin*** , unlike bacteriorhodopsin, transports protons at pH below the pKa of the proton acceptor, and this transport is in the reverse direction. We have investigated the photocycle of ***proteorhodopsin*** at such low pH. At pH 5, three spectrally distinct intermediates K, L, and N, and another spectrally silent one, PR', could be identified, but a deprotonated Schiff base contg. an M-like intermediate characteristic of proton pumping activity does not accumulate. All the reactions between the intermediates are close to equil., except the last transition from PR' to PR, when the protein returns to its initial unexcited state in a quasiunidirectional reaction. The elec. signal measurements indicate that although charge motions are detected inside the protein, their net dislocation is zero, indicating that contrary to the earlier reported, at low pH no charged particle is transported across the membrane.

ST   ***proteorhodopsin***   photocycle membrane charge transport
IT   Biological transport
        (hydrogen ion; charge transport across membrane does not occur during
        photochem. reaction cycle of   ***proteorhodopsin***   at low pH)
IT   Rhodopsins
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (***proteorhodopsins*** ; charge transport across membrane does not
        occur during photochem. reaction cycle of   ***proteorhodopsin***   at
        low pH)
IT   Enthalpy
     Entropy
     Free energy
        (temp.-dependent absorption kinetic signals permit anal. of free
        energy, enthalpy, and entropy of   ***proteorhodopsin***   photocycle
        at low pH)
RE.CNT 22   THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN   2003:347288 CAPLUS <<LOGINID::20060726>>
DN   139:48914
ED   Entered STN: 08 May 2003
TI   Proton Transport by   ***Proteorhodopsin***   Requires that the Retinal
     Schiff Base Counterion Asp-97 Be Anionic

AU   Dioumaev, Andrei K.; Wang, Jennifer M.; Balint, Zoltan; Varo, Gyoergy;
     Lanyi, Janos K.
CS   Department of Physiology and Biophysics, University of California, Irvine,
     CA, 92697, USA

SO   Biochemistry (2003), 42(21), 6582-6587
     CODEN: BICHAW; ISSN: 0006-2960
PB   American Chemical Society
DT   Journal
LA   English
CC   6-3 (General Biochemistry)

AB   At pH >7,   ***proteorhodopsin***   functions as an outward-directed
     proton pump in cell membranes, and Asp-97 and Glu-108, the homologs of the
     Asp-85 and Asp-96 in bacteriorhodopsin, are the proton acceptor and donor
     to the retinal Schiff base, resp. It was reported, however [Friedrich, T.
     et al. (2002) J. Mol. Biol., 321, 821-838], that   ***proteorhodopsin***
     transports protons also at pH <7 where Asp-97 is protonated and in the
     direction reverse from that at higher pH. To explore the roles of Asp-97
     and Glu-108 in the proposed pumping with variable vectoriality, we
     compared the photocycles of D97N and E108Q mutants, and the effects of
     azide on the photocycle of the E108Q mutant, at low and high pH. Unlike
     at high pH, at a pH low enough to protonate Asp-97 neither the mutations
     nor the effects of azide revealed evidence for the participation of the
     acidic residues in proton transfer, and as in the photocycle of the
     wild-type protein, no intermediate with unprotonated Schiff base
     accumulated. In view of these findings, and the doubts raised by absence

of charge transfer after flash excitation at low pH, we revisited the question whether transport occurs at all under these conditions. In both oriented membrane fragments and liposomes reconstituted with ***proteorhodopsin*** , we found transport at high pH but not at low pH. Instead, proton transport activity followed the titrn. curve for Asp-97, with an apparent pKa of 7.1, and became zero at the pH where Asp-97 is fully protonated.

ST proton transfer ***proteorhodopsin*** retina retinal Schiff base aspartic acid

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***proteorhodopsin*** ; proton transport by ***proteorhodopsin*** requires that retinal Schiff base counterion Asp97 residue be anionic)

IT Proton transfer
(proton transport by ***proteorhodopsin*** requires that retinal Schiff base counterion Asp97 residue be anionic)

IT Schiff bases
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proton transport by ***proteorhodopsin*** requires that retinal Schiff base counterion Asp97 residue be anionic)

IT 56-84-8, L-Aspartic acid, biological studies 116-31-4, all-trans-Retinal 14343-69-2, Azide
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proton transport by ***proteorhodopsin*** requires that retinal Schiff base counterion Asp97 residue be anionic)

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 38 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:294076 CAPLUS <<LOGINID::20060726>>
DN 139:129560
ED Entered STN: 16 Apr 2003
TI Diversification and spectral tuning in marine ***proteorhodopsins***
AU Man, Dikla; Wang, Weiwu; Sabehi, Gazalah; Aravind, L.; Post, Anton F.; Massana, Ramon; Spudich, Elena N.; Spudich, John L.; Beja, Oded
CS Department of Biology, Technion-Israel Institute of Technology, Haifa, 32000, Israel
SO EMBO Journal (2003), 22(8), 1725-1731
CODEN: EMJODG; ISSN: 0261-4189
PB Oxford University Press
DT Journal
LA English
CC 6-3 (General Biochemistry)
Section cross-reference(s): 3, 10
AB ***Proteorhodopsins*** , ubiquitous retinylidene photoactive proton pumps, were recently discovered in the cosmopolitan uncultured SAR86

bacterial group in oceanic surface waters. Two related ***proteorhodopsin*** families were found that absorb light with different absorption maxima, 525 nm (green) and 490 nm (blue), and their distribution was shown to be stratified with depth. Using structural modeling comparisons and mutagenesis, we report here on a single amino acid residue at position 105 that functions as a spectral tuning switch and accounts for most of the spectral difference between the two pigment families. Furthermore, looking at natural environments, we found novel ***proteorhodopsin*** gene clusters spanning the range of 540-505 nm and contg. changes in the same identified key switch residue leading to changes in their absorption maxima. The results suggest a simultaneous diversification of green ***proteorhodopsin*** and the new key switch variant pigments. Our observations demonstrate that this single-residue switch mechanism is the major determinant of ***proteorhodopsin*** wavelength regulation in natural marine environments.

ST ***proteorhodopsin*** marine environment spectral tuning; marine microorganism ***proteorhodopsin*** sequence diversity spectral tuning

IT Environment
(marine, light level adaptation; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT Evolution
(mol., phylogenetic anal. of ***proteorhodopsin*** sequences; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT DNA sequences
(of ***proteorhodopsin*** genes; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT Protein sequences
(of ***proteorhodopsins*** ; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT Conformation
(predicted by homol. modeling; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT Rhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsins*** ; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT Marine microorganism
UV and visible spectra
(sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT Adaptation, microbial
(to light levels; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT 567403-01-4 567403-02-5 567403-03-6 567403-04-7 567403-05-8
567403-06-9 567403-07-0 567403-08-1 567403-09-2 567403-10-5
567403-11-6 567403-12-7 567403-13-8 567403-14-9 567403-15-0
567403-16-1 567403-17-2 567403-18-3 567403-19-4 567403-20-7
567403-21-8 567403-22-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

IT 495706-48-4, GenBank AY210898 495706-49-5, GenBank AY210899
495706-50-8, GenBank AY210900 495706-51-9, GenBank AY210901
495706-52-0, GenBank AY210902 495706-53-1, GenBank AY210903
495706-54-2, GenBank AY210904 495706-55-3, GenBank AY210905
495706-56-4, GenBank AY210906 495706-57-5, GenBank AY210907
495706-58-6, GenBank AY210908 495706-59-7, GenBank AY210909
495706-60-0, GenBank AY210910 495706-61-1, GenBank AY210911
495706-62-2, GenBank AY210912 495706-63-3, GenBank AY210913
495706-64-4, GenBank AY210914 495706-65-5, GenBank AY210915
495706-66-6, GenBank AY210916 495706-67-7, GenBank AY210917
495706-68-8, GenBank AY210918 495706-69-9, GenBank AY210919
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; sequence diversity and spectral tuning in marine ***proteorhodopsins***)

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L1 ANSWER 39 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:88892 CAPLUS <<LOGINID::20060726>>
DN 138:299327
ED Entered STN: 05 Feb 2003
TI Characterization of the photochemical reaction cycle of ***proteorhodopsin***
AU Varo, Gyorgy; Brown, Leonid S.; Lakatos, Melinda; Lanyi, Janos K.
CS Institute of Biophysics, Biological Research Center of the Hungarian Academy of Sciences, Szeged, H-6701, Hung.
SO Biophysical Journal (2003), 84(2, Pt. 1), 1202-1207
CODEN: BIOJAU; ISSN: 0006-3495
PB Biophysical Society
DT Journal
LA English
CC 6-1 (General Biochemistry)
AB Absorption changes in the photocycle of the recently described retinal protein, ***proteorhodopsin*** , are analyzed. The transient spectra at pH 9.5, where it acts as a light-driven proton pump, reveal the existence of three spectrally different intermediates, K, M, and N, named in analogy with the photointermediates of bacteriorhodopsin. Model anal. based on time-dependent absorption kinetic signals at four wavelengths suggested the existence of two more spectrally silent intermediates and lead to a sequential reaction scheme with five intermediates, K, M1, M2, N, and PR', before decay to the initial state PR. An L-like intermediate was not obsd., probably for kinetic reasons. By measuring the light-generated elec. signal of an oriented sample, the electrogenicity of each intermediate could be detd. The electrogenicities of the first three intermediates (K, M1, and M2) have small neg. value, but the last three components, corresponding to the N and PR' intermediates and PR, are pos. and two-orders-of-magnitude larger. These states give the major contributions to the proton translocation across the membrane. The energetic scheme of the photocycle was calcd. from the temp.-dependence of the absorption kinetic signals.
ST photochem cycle ***proteorhodopsin*** proton transport thermodn
IT Electric current
(biol.; characterization of photochem. reaction cycle of ***proteorhodopsin***)

IT Enthalpy
Entropy
Free energy
Light
Membrane, biological
(characterization of photochem. reaction cycle of ***proteorhodopsin***)
IT Biological transport
(hydrogen ion; characterization of photochem. reaction cycle of ***proteorhodopsin***)
IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsin*** , intact and intermediate states K, M, and N; characterization of photochem. reaction cycle of ***proteorhodopsin***)
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L1 ANSWER 40 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:661588 CAPLUS <<LOGINID::20060726>>
DN 137:365154
ED Entered STN: 03 Sep 2002
TI ***Proteorhodopsin*** is a Light-driven Proton Pump with Variable Vectoriality

AU Friedrich, Thomas; Geibel, Sven; Kalmbach, Rolf; Chizhov, Igor; Ataka, Kenichi; Heberle, Joachim; Engelhard, Martin; Bamberg, Ernst
CS Department of Biophysical Chemistry, Max-Planck-Institute of Biophysics, Frankfurt am Main, D-60596, Germany

SO Journal of Molecular Biology (2002), 321(5), 821-838
CODEN: JMOBAK; ISSN: 0022-2836
PB Elsevier Science Ltd.

DT Journal
LA English
CC 6-3 (General Biochemistry)
Section cross-reference(s): 10

AB ***Proteorhodopsin*** , a homolog of archaeal bacteriorhodopsin (BR), belongs to a newly identified family of retinal proteins from marine bacteria, which could play an important role in the energy balance of the biosphere. We cloned the cDNA sequence of ***proteorhodopsin*** by chem. gene synthesis, expressed the protein in Escherichia coli cells, purified and reconstituted the protein in its functional active state. The photocycle characteristics were detd. by time-resolved absorption and Fourier transform IR (FT-IR) spectroscopy. The pH-dependence of the absorption spectrum indicates that the pKa of the primary acceptor of the Schiff base proton (Asp97) is 7.68. Generally, the photocycle of ***proteorhodopsin*** is similar to that of BR, although an L-like photocycle intermediate was not detectable. Whereas at pH>7 an M-like intermediate is formed upon illumination, at pH 5 no M-like intermediate could be detected. As the photocycle kinetics do not change between the acidic and alk. state of ***proteorhodopsin*** , the only difference between these two forms is the protonation status of Asp97. This is corroborated by time-resolved FT-IR spectroscopy, which demonstrates that

proton transfer from the retinal Schiff base to Asp97 is obsd. at alk. pH, but the other vibrational changes are essentially pH-independent. After reconstitution into proteoliposomes, light-induced proton currents of ***proteorhodopsin*** were measured in a compd. membrane system where proteoliposomes were adsorbed to planar lipid bilayers. Our results show that ***proteorhodopsin*** is a light-driven proton pump with characteristics similar to those of BR at alk. pH. However, at acidic pH, the direction of proton pumping is inverted. Complementary expts. were carried out on ***proteorhodopsin*** expressed heterologously in Xenopus laevis oocytes under voltage clamp conditions. The following results were obtained: (1) at alk. pH, ***proteorhodopsin*** mediates outwardly directed proton pumping like BR; (2) the direction of proton pumping can be inverted, when Asp97 is protonated; (3) the current can be inverted by changes of the polarity of the applied voltage; and (4) the light intensity-dependence of the photocurrents leads to the conclusion that the alk. form of ***proteorhodopsin*** shows efficient proton pumping after sequential excitation by two photons.

ST ***proteorhodopsin*** light driven proton pump direction acidic alk pH

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***Proteorhodopsin*** ; ***proteorhodopsin*** is a light-driven proton pump with variable vectoriality)

IT pH
(dependent; the direction of ***proteorhodopsin*** proton pumping depends of pH and protonation status of proton-acceptor, Asp97)

IT Photocurrent
(direction and light intensity-dependence of ***proteorhodopsin*** photocurrents)

IT Biological transport
(hydrogen ion; the direction of ***proteorhodopsin*** proton pumping depends of pH and protonation status of proton-acceptor, Asp97)

IT Transport proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proton pump; ***proteorhodopsin*** is a light-driven proton pump with variable vectoriality)

IT Proton transfer
(the direction of ***proteorhodopsin*** proton pumping depends of pH and protonation status of proton-acceptor, Asp97)

IT Photoexcitation
(two-photon; direction and light intensity-dependence of ***proteorhodopsin*** photocurrents)

IT 56-84-8, L-Aspartic acid, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(residue 97; the direction of ***proteorhodopsin*** proton pumping depends of pH and protonation status of proton-acceptor, Asp97)

IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(the direction of ***proteorhodopsin*** proton pumping depends of pH and protonation status of proton-acceptor, Asp97)

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L1 ANSWER 41 OF 45 CAPLUS
AN 2002:446596 CAPLUS <<LOGINID::20060726>>
DN 137:197216
ED Entered STN: 14 Jun 2002
TI Detection of fast light-activated H+ release and M intermediate formation from ***proteorhodopsin***
AU Krebs, Richard A.; Alexiev, Ulrike; Partha, Ranga; DeVita, Anne Marie; Braiman, Mark S.
CS Chemistry Department, Syracuse University, Syracuse, NY, 13244-4100, USA
SO BMC Physiology [online computer file] (2002), 2, No pp. given
CODEN: BPMHCV; ISSN: 1472-6793
URL: http://www.biomedcentral.com/1472-6793/2/5
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
CC 6-3 (General Biochemistry)
AB Background: ***Proteorhodopsin*** (pR) is a light-activated proton pump homologous to bacteriorhodopsin and recently discovered in oceanic .gamma.-proteobacteria. One perplexing difference between these two proteins is the absence in pR of homologs of bR residues Glu-194 and Glu-204. These two residues, along with Arg-82, have been implicated in light-activated fast H+ release to the extracellular medium in bR. It is therefore uncertain that pR carries out its physiol. activity using a mechanism that is completely homologous to that of bR. Results: A pR purifn. procedure is described that utilizes Phenylsepharose and hydroxylapatite columns and yields 85% (wt./wt.) purity. Through SDS-PAGE of the pure protein, the mol. wt. of E-coli-produced pR was detd. to be 36,000, approx. 9,000 more than the 27,000 predicted by the DNA sequence. Post-translational modification of one or more of the cysteine residues accounts for 5 kDa of the wt. difference as measured on a cys-less pR mutant. At pH 9.5 and in the presence of octylglucoside and dihepatanoylphosphotidylcholine, flash photolysis results in fast H+ release and a 400-nm absorbing (M-like) photoproduct. Both of these occur with a similar rise time (4-10 .mu.s) as reported for monomeric bR in detergent. Conclusions: The presence of fast H+ release in pR indicates that either different groups are responsible for fast H+ release in pR and bR (i.e. that the H+ release group is not highly conserved); or, that the

H+ release group is conserved and is therefore likely Arg-94 itself in pR (and Arg-82 in bR, correspondingly).

ST ***proteorhodopsin*** bacteriorhodopsin hydrogen release

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(fast H release in pR and bR)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***proteorhodopsin*** ; detection of fast light-activated H+ release and M intermediate formation from ***proteorhodopsin***)

IT 12408-02-5, Hydrogen ion, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(transport; fast H release in pR and bR)

RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD

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AN 2002:259417 CAPLUS <<LOGINID::20060726>>

DN 136:397567

ED Entered STN: 09 Apr 2002

TI Proton Transfers in the Photochemical Reaction Cycle of ***Proteorhodopsin***

AU Dioumaev, Andrei K.; Brown, Leonid S.; Shih, Jennifer; Spudich, Elena N.; Spudich, John L.; Lanyi, Janos K.

CS Department of Physiology Biophysics, University of California, Irvine, CA, 92697, USA

SO Biochemistry (2002), 41(17), 5348-5358
CODEN: BICHAW; ISSN: 0006-2960

PB American Chemical Society

DT Journal

LA English

CC 6-3 (General Biochemistry)

AB The spectral and photochem. properties of ***proteorhodopsin*** (PR) were detd. to compare its proton transport steps to those of bacteriorhodopsin (BR). Static and time-resolved measurements on wild-type PR and several mutants were done in the visible and IR (FTIR and FT-Raman). Assignment of the obsd. C:O stretch bands indicated that Asp-97 and Glu-108 serve as the proton acceptor and donor, resp., to the retinal Schiff base, as do the residues at corresponding positions in BR, but there are numerous spectral and kinetic differences between the two proteins. There is no detectable dark-adaptation in PR, and the chromophore contains nearly entirely all-trans retinal. Because the pKa of Asp-97 is relatively high (7.1), the proton-transporting photocycle is produced only at alk. pH. It contains at least seven transient states with decay times in the range from 10 .mu.s to 200 ms, but the anal. reveals only three distinct spectral forms. The first is a red-shifted K-like state. Proton release does not occur during the very slow (several milliseconds) rise of the second, M-like, intermediate, consistent with lack of the residues facilitating extracellular proton release in BR.

Proton uptake from the bulk, presumably on the cytoplasmic side, takes place prior to release (.tau. .apprx. 2 ms), and coincident with reprotonation of the retinal Schiff base. The intermediate produced by this process contains 13-cis retinal as does the N state of BR, but its absorption max. is red-shifted relative to PR (like the O state of BR). The decay of this N-like state is coupled to reisomerization of the retinal to all-trans, and produces a state that is O-like in its C-C stretch bands, but has an absorption max. apparently close to that of unphotolyzed PR.

ST ***proteorhodopsin*** bacteriorhodopsin retinal proton transfer photocycle kinetics

IT Proton transfer
Protonation
(proton transfers in the photochem. reaction cycle of ***proteorhodopsin***)

IT Bacteriorhodopsins
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); BIOL (Biological study); PROC (Process)
(proton transfers in the photochem. reaction cycle of ***proteorhodopsin***)

IT 116-31-4, all-trans-Retinal 472-86-6, 13-cis-Retinal
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); BIOL (Biological study); PROC (Process)
(proton transfers in the photochem. reaction cycle of ***proteorhodopsin***)

RE.CNT 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 43 OF 45 CAPLUS
AN 2001:816865 CAPLUS <<LOGINID::20060726>>
DN 135:353852
ED Entered STN: 09 Nov 2001
TI Light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes
IN Delong, Edward F.; Beja, Oded
PA Monterey Bay Aquarium Research Institute, USA
SO PCT Int. Appl., 460 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 10, 52
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001083701	A2	20011108	WO 2001-US14394	20010502
	WO 2001083701	C1	20030612		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CO, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 2003104375	A1	20030605	US 2001-847513	20010501
	AU 2001061181	A5	20011112	AU 2001-61181	20010502
	EP 1337552	A2	20030827	EP 2001-935053	20010502
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
	JP 2004521604	T2	20040722	JP 2001-580311	20010502
PRAI	US 2000-201602P	P	20000503		
	WO 2001-US14394	W	20010502		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2001083701	ICM	C12N
	IPCI	C12N [ICM,7]
	IPCR	C07K0014-195 [I,A]; C07K0014-195 [I,C*]
	ECLA	C07K014/195
US 2003104375	IPCI	C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C07K0014-195 [ICS,7]; C12N0015-74 [ICS,7]
	IPCR	C07K0014-195 [I,A]; C07K0014-195 [I,C*]
	NCL	435/006.000
	ECLA	C07K014/195
AU 2001061181	IPCR	C07K0014-195 [I,A]; C07K0014-195 [I,C*]
EP 1337552	IPCI	C07K0014-00 [ICM,7]
	IPCR	C07K0014-195 [I,A]; C07K0014-195 [I,C*]
JP 2004521604	IPCI	C12N0015-09 [ICM,7]; C12M0001-00 [ICS,7]; C12P0021-02 [ICS,7]; C12Q0001-68 [ICS,7]
	IPCR	C07K0014-195 [I,A]; C07K0014-195 [I,C*]
	FTERM	4B024/AA17; 4B024/BA80; 4B024/CA02; 4B024/DA20;

4B024/GA30; 4B029/AA01; 4B029/AA27; 4B029/BB15; 4B029/CC11; 4B063/QA01; 4B063/QA18; 4B063/QQ06; 4B063/QQ43; 4B063/QR08; 4B063/QR32; 4B063/QR42; 4B063/QR62; 4B063/QS25; 4B063/QX02; 4B064/AG01; 4B064/CA19; 4B064/CC24; 4B064/CE20; 4B064/DA20

AB A light-driven energy generation system using ***proteorhodopsin*** is provided. ***Proteorhodopsin*** sequences were retrieved and amplified from naturally occurring members of proteobacteria using ***proteorhodopsin*** -specific PCR primers. The gene and encoded protein sequences are provided for 30 different genes and variants are provided. ***Proteorhodopsin*** sequences were placed in expression vectors for prodn. of ***proteorhodopsin*** proteins in a host, for instance, Escherichia coli and other bacteria. The system also includes a light source and a source of retinal, that allows the system to convert light into biochem. energy. The generated biochem. energy could be mediated into elec. energy by a mediator.

ST ***proteorhodopsin*** light driven energy generation; sequence ***proteorhodopsin*** gene marine bacteria; cloning ***proteorhodopsin*** membrane photoenergy generation

IT Genetic vectors
(BAC (bacterial artificial chromosome), gene cloning from; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT Genomic library
(gene cloning from; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT Bacteria (Eubacteria)
Bacterioplankton
Cell membrane
DNA sequences
Energy converters
Marine bacteria
Membrane, biological
Molecular cloning
PCR (polymerase chain reaction)
Photoinduced energy transfer
Protein sequences
(light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT Gene, microbial
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT Bacteriorhodopsins
RL: BPN (Biosynthetic preparation); NUU (Other use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT Escherichia coli
(recombinant host; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT 372993-51-6 372993-52-7
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PCR primer for gene isolation; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT 372993-82-3 372993-83-4 372993-84-5 372993-85-6 372993-86-7
372993-87-8 372993-88-9 372993-89-0 372993-90-3 372993-91-4
372993-92-5 372993-93-6 372993-94-7 372993-95-8 372993-96-9
372993-97-0 372993-98-1 372993-99-2 372994-00-8 372994-01-9
372994-02-0 372994-03-1 372994-04-2 372994-05-3 372994-06-4
372994-07-5 372994-08-6
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); NUU (Other use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT 372993-50-5 372993-53-8 372993-54-9 372993-55-0 372993-56-1
372993-57-2 372993-58-3 372993-59-4 372993-60-7 372993-61-8
372993-62-9 372993-63-0 372993-64-1 372993-65-2 372993-66-3
372993-67-4 372993-68-5 372993-69-6 372993-70-9 372993-71-0

372993-72-1   372993-73-2   372993-74-3   372993-75-4   372993-76-5
372993-77-6   372993-78-7   372993-79-8   372993-80-1   372993-81-2
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT 372994-90-6, 7: PN: WO0183701 SEQID: 6 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

IT 372994-91-7
RL: PRP (Properties)
(unclaimed protein sequence; light-driven energy generation using ***proteorhodopsin*** cloned from various marine bacterial genes)

L1 ANSWER 44 OF 45 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:459257 CAPLUS <<LOGINID::20060726>>
DN 135:170332
ED Entered STN: 26 Jun 2001
TI ***Proteorhodopsin*** phototrophy in the ocean
AU Beja, Oded; Spudich, Elena N.; Spudich, John L.; Leclerc, Marion; DaLong, Edward F.
CS Monterey Bay Aquarium Research Institute, Moss Landing, CA, 95039, USA
SO Nature (London, United Kingdom) (2001), 411(6839), 786-789
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
CC 61-1 (Water)
Section cross-reference(s): 3

AB ***Proteorhodopsin*** , a retinal-contg. integral membrane protein that functions as a light-driven proton pump, was discovered in the genome of an uncultivated marine bacterium; however, the prevalence, expression and genetic variability of this protein in native marine microbial populations remain unknown. We report photoactive ***proteorhodopsin*** presence in oceanic surface waters. We provide evidence of an extensive family of globally distributed ***proteorhodopsin*** variants. The protein pigments comprising this rhodopsin family seem to be spectrally tuned to different habitats, absorbing light at different wave-lengths in accordance with light available in the environment. Our data suggest that ***proteorhodopsin*** -based phototrophy is a globally significant oceanic microbial process.

ST ***proteorhodopsin*** phototropism ocean; marine bacteria ***proteorhodopsin*** gene cloning sequence

IT Gene, microbial
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(for ***proteorhodopsins*** of uncultured marine bacteria, cloning and sequences of; ***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

IT DNA sequences
(for ***proteorhodopsins*** of uncultured marine bacteria; ***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(membrane, integral, ***Proteorhodopsin*** ; ***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

IT Protein sequences
(of ***proteorhodopsins*** of uncultured marine bacteria; ***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

IT Marine bacteria
Phototropism
Seawater
(***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

IT 353580-30-0   353580-31-1   353580-32-2   353580-33-3   353580-34-4

353580-35-5 353580-36-6 353580-37-7 353580-38-8 353580-39-9
353580-40-2 353580-41-3 353580-42-4 353580-43-5 353580-44-6
353580-45-7 353580-46-8 353580-47-9 353580-48-0 353580-49-1
353580-50-4 353580-51-5 353580-52-6 353580-53-7 353580-54-8
353580-55-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; ***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

IT 330780-02-4, GenBank AF349976 330780-03-5, GenBank AF349977
330780-04-6, GenBank AF349978 330780-05-7, GenBank AF349979
330780-06-8, GenBank AF349980 330780-07-9, GenBank AF349981
330780-08-0, GenBank AF349982 330780-09-1, GenBank AF349983
330780-10-4, GenBank AF349984 330780-11-5, GenBank AF349985
330780-12-6, GenBank AF349986 330780-13-7, GenBank AF349987
330780-14-8, GenBank AF349988 330780-15-9, GenBank AF349989
330780-16-0, GenBank AF349990 330780-17-1, GenBank AF349991
330780-18-2, GenBank AF349992 330780-19-3, GenBank AF349993
330780-20-6, GenBank AF349994 330780-21-7, GenBank AF349995
330780-22-8, GenBank AF349996 330780-23-9, GenBank AF349997
330780-24-0, GenBank AF349998 330780-25-1, GenBank AF349999
330780-26-2, GenBank AF350000 330780-27-3, GenBank AF350001
330780-28-4, GenBank AF350002 330780-29-5, GenBank AF350003
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; ***proteorhodopsin*** distribution and variation and phototrophy in ocean surface waters)

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L1 ANSWER 45 OF 45 CAPLUS
AN 1980:402517 CAPLUS <<LOGINID::20060726>>
DN 93:2517
ED Entered STN: 12 May 1984
TI Chromatography, delipidation and formation of recombinants of walleyed pollack rhodopsin
AU Shukolyukov, S. A.; Kalishevich, O. O.; Tyurin, V. A.; Dikarev, V. P.; Korchagin, V. P.; Kotelevtsev, S. V.; Kagan, V. E.; Mitsner, B. I.; Sokolova, N. A.
CS Far East. Sci. Cent., Inst. Mar. Biol., Vladivostok, USSR
SO Biokhimiya (Moscow) (1980), 45(3), 398-407
CODEN: BIOHAO; ISSN: 0006-307X
DT Journal
LA Russian
CC 6-3 (General Biochemistry)
AB Dodecyltrimethylammonium bromide (100 mM) used to solubilize walleyed pollack rhodopsin caused a rapid spontaneous bleaching of the original

prepn. Chromatog. of the rhodopsin solubilized by 100 mM N',N'-dimethyldodecylamine-N-oxide gave a 30-50% yield to unbleached, dark prepns. The rest of the prepn. was delipidated down to 5-40 mol of phospholipid/mol of rhodopsin and was almost completely bleached and aggregated. Rhodopsin was irreversibly adsorbed on hydroxylapatite, but was eluted from a column of agarose A before the unbleached dark prepn. Promising results were obtained after rhodopsin solubilization in 1-2% Na cholate. Chromatog. of the protein with this detergent on agarose A gave an 80-90% yield of the unbleached dark prepn. and a considerable removal of lipids (.ltoreq.1-5 mol phospholipids/mol enzyme) and a slight bleaching. However, the regeneration capacity and thermal stability of such delipidated prepns. decreased almost 2-fold as compared to the original prepn. contg. .ltoreq.100 mol phospholipids/mol rhodopsin. Removal of the main bulk of Na cholate by dialysis at 0-2.degree. and simultaneous administration of natural and synthetic phospholipids gave detergent-free recombinants (proteoliposomes) of the protein. Administration of lipids after removal of the detergent increased the thermal stability of rhodopsin in the recombinants up to values typical for the enzyme from the native membranes of rod outer segments.

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ST   rhodopsin proteoliposome reconstitution
IT   Rhodopsins
     RL: BIOL (Biological study)
        (proteoliposomes contg., of walleyed pollock, reconstitution of)
IT   Phospholipids
     RL: BIOL (Biological study)
        (rhodopsin of walleyed pollock reconstitution with)
IT   Theragra chalcogramma
        (rhodopsin of, proteoliposome reconstitution from)
IT   Liposome
        (  ***proteo***  -,   ***rhodopsin***  -contg., reconstitution of)


=> d his

     (FILE 'HOME' ENTERED AT 09:17:39 ON 26 JUL 2006)

     FILE 'CAPLUS' ENTERED AT 09:17:54 ON 26 JUL 2006
L1           45 S PROTEORHODOPSIN OR PROTEO(2W)RHODOPSIN

=> log y
COST IN U.S. DOLLARS                              SINCE FILE     TOTAL
                                                       ENTRY   SESSION
FULL ESTIMATED COST                                   142.18    142.39

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)        SINCE FILE     TOTAL
                                                       ENTRY   SESSION
CA SUBSCRIBER PRICE                                   -32.25    -32.25

STN INTERNATIONAL LOGOFF AT 09:19:44 ON 26 JUL 2006
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DERWENT-ACC-NO: 2001-640014

DERWENT-WEEK: 200535

TITLE: Fraud-proof data carrier useful for security, e.g. banknote or check, contains photochromic substance converted from one stable isomer to another by light, embedded in substrate transmitting conversion and read-out light

INVENTOR: BROSOW, J

PATENT-ASSIGNEE: MIB MUNICH INNOVATIVE BIOMATERIALS GMBH[MIBMN] , BROSOW J[BROSI]

PRIORITY-DATA: 1999DE-1061841 (December 21, 1999) , 2001WO-EP07315 (June 27, 2001) , 2001EP-0960397 (June 27, 2001) , 2001AU-0281901 (June 27, 2001) , 2004US-0481928 (August 8, 2004)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
DE 19961841 A1	June 28, 2001	N/A	006	B44F 001/12
WO 2003002351 A1	January 9, 2003	G	000	B41M 003/14
EP 1404526 A1	April 7, 2004	G	000	B41M 003/14
AU 2001281901 A1	March 3, 2003	N/A	000	B41M 003/14
US 20050024955 A1	February 3, 2005	N/A	000	G11C 007/00

DESIGNATED-STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM

TR TT TZ UA UG US UZ VN YU ZA ZW AT BE CH CY DE DK EA ES FI FR GB GH
GM GR IE
IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW AL AT BE CH CY
DE DK ES
FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

APPLICATION-DATA:

PUB-NO	APPL-DESCRIPTOR	APPL-NO
APPL-DATE		
DE 19961841A1	N/A	1999DE-1061841
December 21, 1999		
WO2003002351A1	N/A	2001WO-EP07315
June 27, 2001		
EP 1404526A1	N/A	2001EP-0960397
June 27, 2001		
EP 1404526A1	N/A	2001WO-EP07315
June 27, 2001		
EP 1404526A1	Based on	WO2003002351
N/A		
AU2001281901A1	N/A	2001AU-0281901
June 27, 2001		
AU2001281901A1	N/A	2001WO-EP07315
June 27, 2001		
AU2001281901A1	Based on	WO2003002351
N/A		
US20050024955A1	N/A	2001WO-EP07315
June 27, 2001		
US20050024955A1	N/A	2004US-0481928
August 8, 2004		

INT-CL (IPC): B41M003/14, B44F001/12 , G07D007/12 , G11C007/00

ABSTRACTED-PUB-NO: DE 19961841A

BASIC-ABSTRACT:

NOVELTY - In a fraud-proof data carrier material with a substrate (I) and a photochromic substance (II), which can be converted by irradiation with light from a first state (IIA) to isomeric second state(s) (IIB) that can be distinguished from (IIA) by irradiation with light, (a) both states have long-term stability; (b) (I) has sufficient transparency for the wavelengths of light used for converting (IIA) to (IIB) and distinguishing these; and (c) (II) is embedded in (I).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for (a) apparatus
for testing this material; (b) apparatus for inscribing the data; (c) a method
of inscribing binary coded data, in which both binary values 0 and 1 are
recorded by the 2 states of (II) in a predetermined raster.

USE - The data carrier preferably is a security (claimed), e.g. banknote or
check.

ADVANTAGE - In existing banknotes printed with photochromic inks, the print is
permanently visible and does not meet security standards, as forgery is
possible with current copying methods. Embedding the photochromic substance in
the substrate gives better security. The technical cost makes it practically
impossible to forge the special doped substrate. Also, the highly-developed
laser method needed for inscribing data, especially as codes, cannot be
operated by forgers, although the unit cost is very low for mass production by
authorized manufacturers.

DESCRIPTION OF DRAWING(S) - The drawing shows a banknote.

Banknote of paper doped with bacteriorhodopsin, which is generally invisible to
the naked eye 1

Localized points converted from stable ground state bR to stable, isomeric
Q-state by irradiation with green and red light 2

Coded or uncoded position data, e.g. optically-readable print 3

CHOSEN-DRAWING: Dwg.1/2

TITLE-TERMS: FRAUD PROOF DATA CARRY USEFUL SECURE BANKNOTE CHECK CONTAIN
PHOTOCHROMIC SUBSTANCE CONVERT ONE STABILISED ISOMER LIGHT EMBED
SUBSTRATE TRANSMIT CONVERT READ LIGHT

DERWENT-CLASS: G05 P75 P78 T04 T05

CPI-CODES: G05-F;

EPI-CODES: T04-A02B; T05-J;

SECONDARY-ACC-NO:
CPI Secondary Accession Numbers: C2001-189478
Non-CPI Secondary Accession Numbers: N2001-478462